
MAQ5RE4

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 1 16:48:49 1996; MasPar time 42.82 Seconds

622.612 Million cell updates/sec

Tabular output not generated.

Title: >US-08-462-355-1

Description: (1-1446) from US08462355.seq

Perfect Score: 1446

N.A. Sequence: 1 ATGCGCTTTCTCTGCTGA.....AAAGAAATAGTACACTGTG 1446

Comp: TACCGCAGAAAGACGACACT.....TTTCTTTATCATGTTGACAC

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 30947 seqs, 9219370 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

n-issued

1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93

10:PCT94 11:PCT95

Statistics: Mean 8.992; Variance 4.572; scale 1.967

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	40	2.8	1872	9	PCT-US93-1 Sequence 39, Applicati	1.58e-12
2	38	2.6	2098	9	PCT-US93-1 Sequence 41, Applicati	3.48e-11
3	34	2.4	720	9	PCT-US93-1 Sequence 35, Applicati	1.47e-08
4	32	2.2	1610	10	PCT-US94-1 Sequence 7, Applicatio	2.78e-07
5	32	2.2	1618	10	PCT-US94-1 Sequence 1, Applicatio	2.78e-07
6	32	2.2	1618	10	PCT-US94-1 Sequence 3, Applicatio	2.78e-07
7	29	2.0	120	9	PCT-US93-1 Sequence 3, Applicatio	2.03e-05
8	28	1.9	1567	10	PCT-US94-1 Sequence 16, Applicati	8.21e-05
9	26	1.8	1265	4	US-07-816- Sequence 3, Applicatio	1.26e-03
c 10	24	1.7	105	4	US-07-865- Sequence 13, Applicati	1.75e-02

11	24	1.7	1307	11	PCT-US95-0	Sequence 1, Applicatio	1.75e-02
12	25	1.7	1317	9	PCT-US93-1	Sequence 45, Applicati	4.75e-03
13	25	1.7	1351	4	US-07-816-	Sequence 5, Applicatio	4.75e-03
14	24	1.7	1572	4	US-08-041-	Sequence 5, Applicatio	1.75e-02
15	25	1.7	1737	4	US-08-202-	Sequence 4, Applicatio	4.75e-03
16	25	1.7	1737	10	PCT-US94-0	Sequence 2, Applicatio	4.75e-03
17	23	1.6	105	4	US-07-865-	Sequence 13, Applicati	6.30e-02
18	23	1.6	1634	4	US-07-816-	Sequence 1, Applicatio	6.30e-02
19	23	1.6	1796	4	US-07-816-	Sequence 11, Applicati	6.30e-02
20	22	1.5	84	10	PCT-US94-0	Sequence 25, Applicati	2.20e-01
21	22	1.5	652	8	PCT-US92-0	Sequence 2, Applicatio	2.20e-01
22	21	1.5	1106	11	PCT-US95-0	Sequence 4, Applicatio	7.42e-01
23	21	1.5	1106	8	PCT-US92-0	Sequence 5, Applicatio	7.42e-01
24	21	1.5	1161	9	PCT-US93-1	Sequence 31, Applicati	7.42e-01
25	21	1.5	1176	11	PCT-US95-0	Sequence 2, Applicatio	7.42e-01
26	22	1.5	1200	11	PCT-US95-0	Sequence 1, Applicatio	2.20e-01
27	22	1.5	1200	8	PCT-US92-0	Sequence 1, Applicatio	2.20e-01
28	21	1.5	1244	4	US-07-816-	Sequence 7, Applicatio	7.42e-01
29	22	1.5	1296	4	US-07-816-	Sequence 9, Applicatio	2.20e-01
30	21	1.5	1510	3	US-07-759-	Sequence 4, Applicatio	7.42e-01
31	21	1.5	1748	4	US-08-202-	Sequence 8, Applicatio	7.42e-01
32	21	1.5	1883	4	US-08-202-	Sequence 2, Applicatio	7.42e-01
33	21	1.5	1901	9	PCT-US93-1	Sequence 43, Applicati	7.42e-01
34	21	1.5	1933	10	PCT-US94-0	Sequence 1, Applicatio	7.42e-01
35	21	1.5	2254	9	PCT-US93-1	Sequence 27, Applicati	7.42e-01
36	21	1.5	2830	9	PCT-US93-0	Sequence 1, Applicatio	7.42e-01
37	21	1.5	2830	3	US-07-882-	Sequence 1, Applicatio	7.42e-01
38	20	1.4	1584	8	PCT-US92-0	Sequence 5, Applicatio	2.42e+00
39	20	1.4	3259	11	PCT-US95-0	Sequence 1, Applicatio	2.42e+00
c 40	20	1.4	4100	8	PCT-US92-0	Sequence 3, Applicatio	2.42e+00
c 41	20	1.4	6375	8	PCT-US92-0	Sequence 5, Applicatio	2.42e+00
c 42	20	1.4	6375	8	PCT-US92-0	Sequence 5, Applicatio	2.42e+00
43	20	1.4	8043	10	PCT-US94-0	Sequence 1, Applicatio	2.42e+00
c 44	20	1.4	8252	4	US-08-046-	Sequence 15, Applicati	2.42e+00
c 45	20	1.4	8252	9	PCT-US93-1	Sequence 15, Applicati	2.42e+00

ALIGNMENTS

RESULT	1
ID	PCT-US93-11153-39 STANDARD, DNA; UNC; 1872 BP.
AC	xxxxxx
DT	01-JAN-1900
DE	Sequence 39, Application PC/TUS9311153.
CC	Sequence 39, Application PC/TUS9311153
CC	GENERAL INFORMATION:
CC	APPLICANT: Godiska, Ronald
CC	APPLICANT: Gray, Patrick W.
CC	APPLICANT: Schweikart, Vicki L.
CC	TITLE OF INVENTION: Novel Seven Transmembrane Receptors
CC	NUMBER OF SEQUENCES: 64
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC	ADDRESSEE: Bicknell
CC	STREET: 6300 Sears Tower, 233 South Wacker Drive
CC	CITY: Chicago
CC	STATE: Illinois
CC	COUNTRY: USA
CC	ZIP: 60606
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/11153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 39:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1872 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 202..1341
SQ Sequence 1872 BP; 328 A; 592 G; 491 C; 456 T; 5 other;
Query Match 2.8%; Score 40; DB 9; Length 1872;
Best Local Similarity 70.0%; Pred. No. 1.58e-12;
Matches 70; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Db 484 TGGCCCTTTGGGACCTCTTCTGCAAGCTCAGAGTACCTACCTCTGCTCAACATGTAC 543
Qy 262 TGGCCCTCAGGAGGTTCTTCTGCAAGCTCAGAGTACCTACCTCTGCTCAACATGT 321
Db 544 GCACGGCTCTTGGCTCAGCGGCTCAGCTCAGCTCGACCGCT 583
Qy 322 GCGAGTGCTTCTGCTTACTGCTGCTGCTGCTGCTGCTGCT 361
RESULT 2
ID PCT-US93-11153-41 STANDARD; DNA; UNC; 2098 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 41, Application PC/TUS9311153.
CC Sequence 41, Application PC/TUS9311153
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC APPLICANT: Schweikart, Vicki L.
CC TITLE OF INVENTION: Novel Seven Transmembrane Receptors
CC NUMBER OF SEQUENCES: 64
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/11153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 41:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2098 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 551..1681
SQ Sequence 2098 BP; 371 A; 594 C; 671 G; 462 T; 0 other;
Query Match 2.6%; Score 38; DB 9; Length 2098;
Best Local Similarity 61.0%; Pred. No. 3.48e-11;
Matches 105; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Db 921 TCACGATGACGCCAGCGTCTGCTTATCAGCGCCATGAGTCTAGACCGCTCAGTCGCGG 980
Qy 311 TCACATGTTGGCAGTGTCTTCTGCTTACTGCGCATAGCCTGGATCGCTGCTTGTGG 370
Db 981 TGGCCCGCCCTTTGTGCCAGAGCTACGACCAAGCGCATGCCCGCGGCTGCTGG 1040
Qy 371 TATTCAGCCAAATCTGGTGTAGAAATCATGCAATGTAGGATGGCCCTGCTATCTGTG 430
Db 1041 CAGGCATCTGGGTGTGCTCTTTCTGCTGGCCACACCCGCTCTCGCGGTACCG 1092
Qy 431 CATGTATCTGGGTGGTGGCTTTTGTGTTGTCATTCCTGTTGCTGTACCG 482
RESULT 3
ID PCT-US93-11153-35 STANDARD; DNA; UNC; 720 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 35, Application PC/TUS9311153.
CC Sequence 35, Application PC/TUS9311153
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC APPLICANT: Schweikart, Vicki L.
CC TITLE OF INVENTION: Novel Seven Transmembrane Receptors
CC NUMBER OF SEQUENCES: 64
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA

CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/11153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856

CC INFORMATION FOR SEQ ID NO: 35:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 720 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 258..719
SQ Sequence 720 BP; 160 A; 176 C; 154 G; 230 T; 0 other;

Query Match 2.4%; Score 34; DB 9; Length 720;
Best Local Similarity 66.0%; Pred. No. 1.47e-08;
Matches 70; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 546 GGAAGTGGCGGACGGGCTCTTCTGTGCAAGGAGCTCTACATGATCCGTCAT 605
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 256 GGACAGTGGCCCTACGGCAGGCTCTATGCAAGCTCATCCCTCCATCATGTCCTCAAC 315

Db 606 ATGCAGTCAAGTCTCTCTGCTCACTTGCATGAGTGTGACCGCT 651
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 316 ATGTTGGCAGTCTCTCTCTTACTGCCATTAGCGTGGATGGCT 361

RESULT 4
ID PCT-US94-10358-7 STANDARD; DNA; UNC; 1610 BP.

AC xxxxxx
DT 01-JAN-1900
DE Sequence 7, Application PC/TUS9410358.
CC Sequence 7, Application PC/TUS9410358
CC GENERAL INFORMATION:

CC APPLICANT:
CC TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10358
CC FILING DATE: Concurrently herewith
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/120.601
CC FILING DATE: 13 SEPTEMBER 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILSON, MARK B.
CC REGISTRATION NUMBER: 37,259
CC REFERENCE/DOCKET NUMBER: INDA005P--
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-3000
CC TELEFAX: (713) 789-2679
CC TELEX: 79-0924

CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1610 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

Query Match 2.2%; Score 32; DB 10; Length 1610;
Best Local Similarity 83.3%; Pred. No. 2.78e-07;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 1092 TGGTGGTGGCTGCTGCTTCATCGCTGCTGCGACTGCCATTCACATTT 1139
||||| ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1139 TGGTGGTGGCTGCTGCTTTCTTCTGCTGCGACTGCCATTCACATTT 1186

RESULT 5
ID PCT-US94-10358-1 STANDARD; DNA; UNC; 1618 BP.

AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9410358.
CC Sequence 1, Application PC/TUS9410358
CC GENERAL INFORMATION:

CC APPLICANT:
CC TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10358
CC FILING DATE: Concurrently herewith
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:


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CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/11153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 120 BP; 26 A; 30 C; 32 G; 32 T; 0 other;
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Query Match 2.0%; Score 29; DB 9; Length 120;
Best Local Similarity 65.3%; Pred.No. 2.03e-05;
Matches 62; Conservative 0; Mismatches 33; Indels 0; Gaps
Db 22 GGACTGTGGAGGACGGGCTCTCTCTGTGCAAGGAGCTCTACATGATCTCCGTCAAT 81
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Qy 256 GGACACTGGCCCTACGGAGGTTCTCTATGCAAGCTCATCCCTCCATCATTTGCTCTCAC 315
||||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 82 ATGCACTGCAGTGTCTCTCTGCTCACTGTCATGAG 116
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Qy 316 ATGTTGGCAGTGTCTCTGCTTACTGCCATTAG 350
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RESULT 8
ID PCT-US94-10358-16 STANDARD; DNA; UNC; 1567 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 16, Application PC/TUS9410358.
CC Sequence 16, Application PC/TUS9410358
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENT IN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC FILING DATE: Concurrently herewith

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CC	CLASSIFICATION:	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: 08/120,601	
CC	FILING DATE: 13 SEPTEMBER 1993	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: WILSON, MARK B.	
CC	REGISTRATION NUMBER: 37,259	
CC	REFERENCE/DOCKET NUMBER: INDA005P---	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (512) 418-3000	
CC	TELEFAX: (713) 789-2679	
CC	TELEX: 79-0924	
CC	INFORMATION FOR SEQ ID NO: 16:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 1567 base pairs	
CC	TYPE: nucleic acid	
CC	STRANDEDNESS: single	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: cDNA	
CC	FEATURE:	
CC	NAME/KEY: CDS	
CC	LOCATION: 173..1273	
SO	Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T; 0 other;	
	Query Match 1.9%; Score 28; DB 10; Length 1567;	
	Best Local Similarity 79.2%; Pred.No. 8.21e-05;	
	Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
Db	949 TCGACTGGTGTGCTAGCTGGCTGTGTTTGTGGCTGTGGAGGCC 996	
Qy	1128 TCGAGTGGCGCTGGTGGTGGTGTCTTTCTTCTGCTGGACTCC 1175	
RESULT	9	
ID	US-07-816-283-3 STANDARD; DNA; UNC; 1265 BP.	
AC	xxxxxx	
DT	01-JAN-1900	
DE	Sequence 3, Application US/07816283.	
CC	Sequence 3, Application US/07816283	
CC	Patent No. 5436155	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Bell, Graeme I.	
CC	APPLICANT: Yamada, Yuichiro	
CC	APPLICANT: Seino, Susumu	
CC	TITLE OF INVENTION: SOMATOSTATIN RECEPTORS	
CC	NUMBER OF SEQUENCES: 12	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Arnold, White & Durkee	
CC	STREET: PO Box 4433	
CC	CITY: Houston	
CC	STATE: Texas	
CC	COUNTRY: USA	
CC	ZIP: 77210	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: Patent In Release #1.0, Version #1.25	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/07/816,283	
CC	FILING DATE: 19911231	
CC	CLASSIFICATION: 435	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: McDaniel, C. Steven	


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CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04464
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wallen III, John W.
CC REGISTRATION NUMBER: 35,403
CC REFERENCE/DOCKET NUMBER: 19202
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1307 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC Sequence 1307 BP; 282 A; 400 C; 306 G; 319 T; 0 other;
SQ
Query Match 1.7%; Score 24; DB 11; Length 1307;
Best Local Similarity 71.4%; Pred.No. 1.75e-02;
Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 974 GTGCTGGCTTCCTGCTGCTGGGCCCTTACCATTCTTTGCTTCCCTCTCGAATT 1029
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QY 1147 GTGGCTGCTCTTTCTGCTGCTGGACCTCATACACATTTGGGGGACTCCTGTCATT 1202

RESULT 12
ID PCT-US93-11153-45 STANDARD; DNA; UNC; 1317 BP.
AC xxxxxx
AD 01-JAN-1900
DT
DE Sequence 45, Application PC/TUS9311153.
CC Sequence 45, Application PC/TUS9311153
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC APPLICANT: Schweikart, Vicki L.
CC TITLE OF INVENTION: Novel Seven Transmembrane Receptors
CC NUMBER OF SEQUENCES: 64
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/11153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302

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CC	CLASSIFICATION:	435
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	JP 085445-1992
CC	FILING DATE:	07-APR-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	JP 101393-1992
CC	FILING DATE:	21-APR-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	JP 027835-1993
CC	FILING DATE:	17-FEB-1993
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Mueller, Douglas P.

RESULT	15	
ID	US-08-202-056-4	STANDARD; DNA; UNC; 1737 BP.
AC	xxxxxx	
DT	01-JAN-1900	
DE	Sequence 4, Application US/08202056.	
CC	Sequence 4, Application US/08202056	
CC	Patent No. 5440021	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Chuntharapai, Anan	
CC	APPLICANT: Hebert, Caroline	
CC	APPLICANT: Kim, Kyung Jin	
CC	APPLICANT: Lee, James	
CC	TITLE OF INVENTION: Antibodies to Human IL-8	Type B Receptor
CC	NUMBER OF SEQUENCES: 8	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Genentech, Inc.	
CC	STREET: 460 Point San Bruno Blvd	
CC	CITY: South San Francisco	
CC	STATE: California	
CC	COUNTRY: USA	
CC	ZIP: 94080	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: patin (Genentech)	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/08/202,056	
CC	FILING DATE: 25-FEB-1994	
CC	CLASSIFICATION: 436	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: 07/677211	
CC	FILING DATE: 29-MAR-1991	

May 1 16:41

US-08-462-355-1.rmi

17

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Love, Richard B.
CC REGISTRATION NUMBER: 34,659
CC REFERENCE/DOCKET NUMBER: 706P3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-5530
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1737 bases
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear

SQ Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other;

Query Match 1.7%; Score 25; DB 4; Length 1737;
Best Local Similarity 61.7%; Pred. No. 4.75e-03;
Matches 66; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

D6 387 GCGAACTGCTACTTTGGAACTTCTATGCAAGGCGATGTCATCTACACAGTCAA 446

||| ||| || ||| ||||| ||||| ||| ||||| |||||

QY 255 GGGACAGTGGCCCTACGGCAGGTTCTATGCAAGCTATGCCCTCATCATTTGCTCTCAA 314

D6 447 CCTCTACAGCAGTGTCTTCATCTGGCCTTCATCATGCTGGACCGCT 493

||| ||| ||||| ||| ||| ||| ||||| |||||

QY 315 CATGTTGGCAGTGTCTTCTCTGTTACTGCGCATTAGCCGTGATCGCT 361

Search completed: Wed May 1 16:49:35 1996
Job time : 46 secs.

DEFINITION Y17h05.r1 Homo sapiens cDNA clone 145305 5' similar to
 SP:BLR1_HUMAN P32302 BURKITT'S LYMPHOMA RECEPTOR ;
 R77881
 EST.
 ACCESSION human clone=145305 library=Soares placenta Nb2HP vector=p7T73D
 KEYWORDS (Pharmacina) with a modified polylinker host=DH10B (ampicillin
 SOURCE resistant) primer=M3RPI RsiteL=Not I Rsite2=Eco RI Female placenta
 obtained at birth (full term). 1st strand cDNA was primed with a
 Not I - oligo(dT) primer [5'
 AACTGGAAGATTCGGCGCGCGAGAAATTTTTTTTTTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacina), digested with Not
 I and cloned into the Not I and Eco RI sites of the modified pT73
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskie,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE

The WashU-Merck EST Project

Unpublished (1995)

COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

High quality sequence stops: 251

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 852991

FEATURES

source Location/Qualifiers
 1..484
 /organism="Homo sapiens"
 /clone="145305"
 /note="human"

BASE COUNT 107 a 117 c 111 g 147 t 2 others

ORIGIN

Query Match 29.1%; Score 421; DB 55; Length 484;
 Best Local Similarity 96.9%; Pred. No. 0.00e+00;
 Matches 469; Conservative 0; Mismatches 8; Indels 7; Gaps 7;

Db 1 taaagcttccctacgctctagcaattcctctacgaagctcagctaccacaaggtt 60
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 Qy 881 TAAAGCTGTTCCGTACGCGTTCTAGCAATTCCTCTACGAGTCTGAGTACCACAAGGTT 940
 |||||
 Db 61 tcacgattattacatttagcccaattcacagatgacgacatcaagtgcacacccctcg 120
 |||||
 Qy 941 TCCAGGATTATTACAATTTAGCCCAATTACAGATGAGCATCAAGTCCCAACACCCCTCG 1000
 |||||
 Db 121 tggcaataacgacatcactaggctagtggttggttcctctgacctgttatcatgatag 180
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 Qy 1001 TGGCAATACGATCATACTAGGCTAGTGGTGGTTTCCTGCTGCCCTCTGTATCATGATAG 1060

Db 181 cctgttacagcttcattctctccgaatgcaaaaggccgcttcgccaagctcagagca 240
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 Qy 1061 CCTGTTACAGCTTCATTGCTTTCGGAATGCAAAAGGGCGCGCTTCCCAAGTCTCAGAGCA 1120
 |||||
 Db 241 aaacctttcgaagtcggcggtggtggtggtggtcttctctgtctgctggaactccatacc 300
 |||||
 Qy 1121 AAACCTTTCCAGTCGGCGTGGTGGTGGCTGCTCTTTCTGCTGCTGCACTCCATACC 1180
 |||||
 Db 301 acatttttgggagtcctgtctcattgcttactgacccagaaacctcccttggggaaaaaacctc 360
 |||||
 Qy 1181 ACATTTG-GGGAGTCCGTG-CATTGCTTACTGACCCAGAACTCCCTTGGGAAAA-CTC 1237
 |||||
 Db 361 tgatgtctgggagtcangtatgcattgctctagcatctgcacattagttgctttaatcc 420
 |||||
 Qy 1238 TGATGCTCGGG-ATCATGTATGCAATGCTCTAGCATCTGCCAAT-AGTTGCTTTATCC 1295
 |||||
 Db 421 ctctcatt-atgcctctcttgggaagatttttagggaggaagcaagg-agtccattcaggg 478
 |||||
 Qy 1296 CTTCCTTTATGCCCTCTTGGGCAAGATTTTAGGAGAGAGGAGGAGTCATTCAGGG 1355
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 Db 479 attt 482
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 Qy 1356 AATT 1359

RESULT 2

LOCUS R92269 471 bp mRNA EST 25-AUG-1995
 DEFINITION yq06g01.r1 Homo sapiens cDNA clone 196176 5'.
 ACCESSION R92269
 KEYWORDS EST.
 SOURCE human clones=196176 library=Soares fetal liver spleen lNFLS
 vector=pT7T3D (Pharmacina) with a modified polylinker host=DH10B
 (ampicillin resistant) primer=M3RPI RsiteL=Pac I Rsite2=Eco RI
 Liver and spleen from a 20 week-post conception male fetus. 1st
 strand cDNA was primed with a Pac I - oligo(dT) primer [5'
 AACTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacina), digested with Pac
 I and cloned into the Pac I and Eco RI sites of the modified pT73
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 471)

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskie,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

TITLE

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 341

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 959809

Location/Qualifiers

FEATURES

source

1..471

/organism="Homo sapiens"

/clone="196176"

/note="human"

<1..>471

mRNA

BASE COUNT

ORIGIN

Query Match 24.8%; Score 358; DB 60; Length 471;

Best Local Similarity 98.2%; Pred. No. 0.00e+00;

Matches 384; Conservative 0; Mismatches 3; Indels 4; Gaps 4;

Db 1 actttatgagatccactagaaacaggctcttgaacattgttcagccgctggag 60

QY 557 ACTTTATGGGATCCACTAGAAAACAGGTCTCTTGAACAACTTGTTCAGCCGCTGGAG 616

Db 61 aaatgaatgagttagatcctctcttccaaacaaatgatccttggacagtc 120

QY 617 AAATGAATGATAGTTAGATCCTCTCTTCCAAACAAATGATCATCTTGGACAGTCC 676

Db 121 ccaatgtcttccaaacctcaaacattcaagacctgtgcagattcaactcctaggggtt 180

QY 677 CCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGATTCACTCCCTAGGGGTT 736

Db 181 ctgatgtttaaacaagtcaaaatctgtattctaatgtatttaaacctgtgatgtgtct 240

QY 737 CTGCTAGGTTAAACAGTCAAAATCTGTATCTTAATGATTTAAACCTGCTGATGTGCT 796

Db 241 cacttaaaatccccagtggttctctattgaagatcacgaaacagccactggataact 300

QY 797 CACCTAAATCCCAAGTGGGTCTCTTATGAGATCAGAAACAGCCCACTGGATAACT 856

Db 301 ctgatgtttctctctactncaatttaagctgttccctagcgtctttagcaattcttc 360

QY 857 CTGATGCTTTTCTCTACT-CATTAAAGCTGTCCCTAGCGCTTCTAGCAATTCCTTC 915

Db 361 tacggagcttgagggttaccacaaggtttnc 391

QY 916 TACG-AGTCT-GAGCT-ACCACAAGGTTTCC 943

RESULT

3

ID HS269192 standard; RNA; EST; 471 BP.

AC R92269;

DT 28-AUG-1995 (Rel. 45, Created)

DE 28-AUG-1995 (Rel. 45, Last updated, Version 1)

DE yq06q01.r1 Homo sapiens cDNA clone 196176 5'.

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.

RN [1]

RP 1-471

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;

RT *The WashU-Merck EST Project*;

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu High quality sequence stops: 341 Source: IMAGE
CC Consortium, LNL This clone is available royalty-free through LNL
CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further
CC information. NCBI gi: 959809

FN Key Location/Qualifiers

FN source 1..471

FT /organism="Homo sapiens"

FT /clone="196176"

FT /note="human"

FT <1..>471

FT mRNA

SQ Sequence 471 BP; 123 A; 115 C; 88 G; 137 T; 8 other;

Query Match 24.8%; Score 358; DB 116; Length 471;

Best Local Similarity 98.2%; Pred. No. 0.00e+00;

Matches 384; Conservative 0; Mismatches 3; Indels 4; Gaps 4;

Db 1 actttatgagatccactagaaacaggctcttgaacattgttcagccgctggag 60

QY 557 ACTTTATGGGATCCACTAGAAAACAGGTCTCTTGAACAACTTGTTCAGCCGCTGGAG 616

Db 61 aaatgaatgagttagatcctctcttccaaacaaatgatccttggacagtc 120

QY 617 AAATGAATGATAGTTAGATCCTCTCTTCCAAACAAATGATCATCTTGGACAGTCC 676

Db 121 ccaatgtcttccaaacctcaaacattcaagacctgtgcagattcaactcctaggggtt 180

QY 677 CCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGATTCACTCCCTAGGGGTT 736

Db 181 ctgatgtttaaacaagtcaaaatctgtattctaatgtatttaaacctgtgatgtgtct 240

QY 737 CTGCTAGGTTAAACAGTCAAAATCTGTATCTTAATGATTTAAACCTGCTGATGTGCT 796

Db 241 cacttaaaatccccagtggttctctattgaagatcacgaaacagccactggataact 300

QY 797 CACCTAAATCCCAAGTGGGTCTCTTATGAGATCAGAAACAGCCCACTGGATAACT 856

Db 301 ctgatgtttctctctactncaatttaagctgttccctagcgtctttagcaattcttc 360

QY 857 CTGATGCTTTTCTCTACT-CATTAAAGCTGTCCCTAGCGCTTCTAGCAATTCCTTC 915

Db 361 tacggagcttgagggttaccacaaggtttnc 391

QY 916 TACG-AGTCT-GAGCT-ACCACAAGGTTTCC 943

RESULT

4

LOCUS T91438 256 bp mRNA EST 22-MAR-1995

DEFINITION ye01d06.r1 Homo sapiens cDNA clone 116459 5'.

ACCESSION T91438

KEYWORDS EST.

SOURCE

human clone=116459 library=Soares fetal liver spleen LNFLS

vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B

(ampicillin resistant) primer=M13R1 Rsite=Pac I Rsite=Eco RI

Liver and spleen from a 20 week-post conception male fetus. 1st

strand cDNA was primed with a Pac I - oligo(dT) primer [5'

AACTGCAAGAAATTAATAAGATCTTTTTTTTTTTT 3'], double-stranded

cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac

I and cloned into the Pac I and Eco RI sites of the modified pT73

vector. Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 256)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 216
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 723351 Location/Qualifiers
source 1..256
/organism="Homo sapiens"
/clone="116459"
/note="human"
BASE COUNT 60 a 70 c 56 g 69 t 1 others
ORIGIN
Query Match 17.2%; Score 248; DB 86; Length 256;
Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 254; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Db 1 agctgtccctagcgtctcagcaattcctcagagctcgtgagctaccacaaaggttcc 60
Qy 884 AGCTGTCCCTAGCGCTTCTAGCAATTCCTCTACAGCTCTGAGCTACCAAGGTTCC 943
Db 61 aggattattacaatttaggcgaattcagatgacgacatcaagtgcccaacccctcgtg 120
Qy 944 AGGATTATTACAATTTAGGCGCAATTCACAGATGACGATCAAGTGCCCAACCCCTCGTG 1003
Db 121 gcataacgacatcactaggtagtggtggttctcgtggtcctggtatcatgatagcc 180
Qy 1004 -CAATAACGATCACATGAGCTAGTGTGGGTTTCTCTGCGCCCTCTTATCATGATGACC 1062
Db 181 tgttcagcttctattgtcttcgaatgcaaaagggcgcttcgcccaagctcagagcaaa 240
Qy 1063 TGTTCAGCTTCAATGTCTTCCGAATGCGAAGGGGGCGCTTCGCCAAGTCTCAGACAAA 1122
Db 241 accttcgagtgccg 256
Qy 1123 ACCTTCGAGTGGCG 1138

RESULT 5
LOCUS T49050 319 bp mRNA EST 08-FEB-1995
DEFINITION yb08e05.r1 Homo sapiens cDNA clone 70592 5'.
ACCESSION T49050
KEYWORDS EST.
SOURCE human clone=70592 library=Stratagene placenta (#937225)

vector=pluescript SK- host=SOIR cells (kanamycin resistant)
primer=M13RP1 Rsite=EcoRI Rsite=XhoI Placental tissue from a
Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCCAGCTTTTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 319)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Other ESTs: yb08e05.s1
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 268
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 650910 Location/Qualifiers
source 1..319
/organism="Homo sapiens"
/clone="70592"
/note="human"
BASE COUNT 85 a 80 c 55 g 99 t
ORIGIN
Query Match 17.0%; Score 246; DB 75; Length 319;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 264; Conservative 0; Mismatches 0; Indels 3; Gaps 3;
Db 11 ctcttgaacaacattgttcagccgcttgagagaaatgaatgataggttagatcctctctt 70
Qy 587 CTCITGAAACATTTTCAGCGCGCTGAGAAATGAATGATAGGTAGTCTCTCTT 646
Db 71 tcacaacaatgatcatccttgagacgtccctcactgtcttccacctcaaacattcaaa 130
Qy 647 TCCAAACAATGATCATCTCTGGACAGTCCCGACTGTCTTCCACCTCAAAATTCAAA 706
Db 131 gacctctgcagattcactccctaggggttctgctaggttaacaagtcaaaatctgtatt 190
Qy 707 GACCTTCTGCAGATTACCTCCCTAGGGGTTCTGCTAGGTTAAACAAGTCAAAATCTGTATT 766
Db 191 ctatgtatttaaacctgctgatgtggtctcacctaaaatccccagtggggttctctatt 250
Qy 767 CTAATGTATTTAAACCTGCTGATGTGCTCTACCTTAAATCCCCAGTGGG-TTTCCTATT 825
Db 251 tgaagatcacggaacacagccactgg 277
Qy 826 -GAAGATCAGC-AAACCAGCCACTGG 850

RESULT 6

May 1 16:40

US-08-462-355-1.rst

9

LOCUS R01558 334 bp mRNA EST 31-MAR-1995
DEFINITION ye79h02.r1 Homo sapiens cDNA clone 123987 5'.
ACCESSION R01558
KEYWORDS EST.
SOURCE human clone=123987 library=Soares fetal liver spleen INFLS

vector=pT7T30 (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RPI Reitel=Pas I Reitel=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGACATTAATAAAGATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 334)

REFERENCE

AUTHORS Hillier,L., Clark,N., Duboue,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 259
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 751294

FEATURES
source
Location/Qualifiers
1..334
/organism="Homo sapiens"
/clone="123987"
/note="human"

BASE COUNT 95 a 68 c 84 g 84 t 3 others

ORIGIN
Query Match 14.7%; Score 212; DB 34; Length 334;
Best Local Similarity 99.5%; Pred. No. 0.00e+00;
Matches 218; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ggaataactctgatgtctctggatcatgtatgtctctagcatctgccaatgttgtct 60
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Qy 1229 GGAATAACTCTGATGTCCTGGATCATGTATGCATTGCTTACGATCTGCCAATAGTTGCT 1288

Db 61 ttaatccctctcttctatgccctcttgggaagaatttttaggaagaagcaggcagtc 120
|||||

Qy 1289 TTAATCCCTCTCTTATGCCCTCTTGGGAAGATTTTAGGAGAAGCAGGCGACTCCA 1348

Db 121 ttcagggaattctggaggcagccttcagtgaggangctcacacgttccaccactgtccc 180
|||||

Qy 1349 TTCAGGGAATTCGAGGCGACGCTTCAGTGAGGA-GCTCACACGCTCCACCCTGCCC 1407

Db 181 tcaacaatgtcatttcagaaagaatagtacaactgtg 19

May 1 16:40

US-08-462-355-1.rst

10

Qy 1408 TCACAACATGTCATTTTCAGAAAGAAATAGTACAACCTGTG 1446
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RESULT 7

LOCUS R58715 297 bp mRNA EST 23-MAY-1995
DEFINITION G4756 Homo sapiens cDNA clone G4756 5' end.
ACCESSION R58715
KEYWORDS EST.

SOURCE human clone=G4756 library=Fetal heart vector=Lambda gt22 host=E. coli Y1090 primer=GGTGGCGACCACTCTCGAGCC Reitel=NotI Reitel=SalI mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a NotI-Oligo dT adaptor-primer. SalI adaptors were ligated, followed by digestion with NotI, for direction cloning into predigested lambda gt22. Method is described in J. Mol. Cell. Cardiol. (1994) 26, 1329-1333).

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)

REFERENCE

AUTHORS Hwang,D.M., Fung,Y.W., Wang,R.X., Laurensen,C.M., Ng,S.H., Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
Analysis of Expressed Sequence Tags (ESTs) from Fetal and Adult Heart cDNA Libraries
Unpublished (1995)

JOURNAL

COMMENT

Contact: Liew CC
Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785650
Email: liewcc@utcc.utoronto.ca.

NCBI gi: 828773

FEATURES
source
Location/Qualifiers
1..297
/organism="Homo sapiens"
/clone="G4756"
/note="human"

BASE COUNT 85 a 63 c 80 g 69 t

ORIGIN
Query Match 5.7%; Score 83; DB 50; Length 297;
Best Local Similarity 91.5%; Pred. No. 3.31e-125;
Matches 108; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Db 1 ttttaggaagagcaggcagtcattcagggaattctggaggcagccttcagtgaggg 60
|||||

Qy 1323 TTTTAGGAGAGAGCAGGCGACTCCATTGAGGGAATTCGGAGGCGCCTTCAGTCGAGGA 1382

Db 61 gg--acagcttccaccactgtccctcaa--caatgtcatttcagagagagatagtag 115
| |||||

Qy 1383 GCTACACGTCCTCCACCCTGTCCTCTCAACAATGTCATTTCAGAAAGAAATAGTAGTA 1440

RESULT 8

LOCUS R06476 349 bp mRNA EST 03-APR-1995
DEFINITION yf09h01.r1 Homo sapiens cDNA clone 126313 5' similar to gb:M60626 FMET-LHE RECEPTOR (HUMAN).
ACCESSION R06476
KEYWORDS EST.

SOURCE human clone=126313 library=Soares fetal liver spleen INF1S vector=pT73D (Pharmacia) with a modified polylinker host=pDH10B (ampicillin resistant) primer=M3Rp1 Reitel-Pac I Reitel-Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGCAGACATTAATTAAGATCTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 I vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 349)

AUTHORS
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: estewartson.wustl.edu
 High quality sequence stops:
 Source: IMAGE Consortium, L

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

```

FEATURES
NCBI gi: 757096
Location/Qualifiers
1..349
/organism="Homo sapiens"
/clone="126313"
/note="human"

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Query Match 4.7%; Score 68; DB 35; Length 349;
Best Local Similarity 64.5%; Pred. No. 9,09e-92;
Matches 151; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Db 5 ggcaacgggcttgatctgggtggctggattccgggatgacacacagtcaccaccatc 64
||||| |||| | ||||| ||||| | |||| | ||||| |||||
Qv 118 GGCAAATGGGCTGCTGTGGTGGTGCGCCCTGCAAGATGACGCCGACAGTCGAACA CAATT 177

Db 65 agttacctgaacctggcgtgagcttctgtttcacctccactttgccattcttcagt 124
+
Qv 178 TGTTTCCTCCACTCAGCTTGCGGGACCTCTCTGCTGCTCTTGCCTTCGTG 237
+ +

Db 125 gtcaggagggccat gggaggacattggcccttcggtcggttcctgtgcgaataatcgctctt 184
| | | | | | | | | | | | | | | | | |
Qv 238 GGTCACTTGGCTCTCCAGGACAGTTGSCCCTACGCAGGTTCCATGAAGGTTCATCCCC 297

Db 185 accatagtagacatcaactgtgtcgaagtgtcttcctgatcgccctcaatttcg 238
 |||||
 QV 298 TCACATATTGTCTCAACATGTTGGCAGTGTTCTCTGCTWACTGCCATTAGC 351

| | |
|------------|---|
| RESULT | 9 |
| LOCUS | R15256 466 bp mRNA EST 13-APR-1995 |
| DEFINITION | yf9rD03.r1 Homo sapiens cDNA clone 29865 5' similar to gb:M67479 G
PROTEIN-COUPLED RECEPTOR RDC1 HOMOLOG (HUMAN).; |

R15256
EST.
human clone=29866 library=Soares infant brain 1N1B vector=Lafmid BA
host=DHI0B (ampicillin resistant) primer=M13Rp1 Rs1ot=Not I
Rs1te2=Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGACAGATTCGGCGCCCGACGAAATTTTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

AUTHORS
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Zannis-Hadjopoulos, D.

TITLE
The WashU-Merck EST Project

JOURNAL
COMMENT
Unpublished (1995)

GDB: G00-402-213

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 303

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI si: 769529

Location/Qualifiers

1.466

```
/organism="Homo sapiens"
```

```
/clone="29866"
```

| BASE COUNT | 94 a | 141 c | 109 g | 119 t | 3 others |
|------------|------|-------|-------|-------|----------|
| ORIGIN | | | | | |

Query Match 2.1%; Score 31; DB 38; Length 466;
Best Local Similarity 65.0%; Pred. No. 8.03e-18;
Matches 67: Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 144 cagtggcccatagggaagctcacgtgcaagtcacacacctcatcttctccatcaacctc 203
||||| ||| ||| ||||| ||| | ||||| |
Qv 259 CAGTGGCCCTACGGCAGGTTCTATGCAGCTCATCCCGTCATCATTTGTCTCAACATG 318

Db 204 ttccgcagcattttcttctcactgcattgcattgaccct 246

[illegible]

RESULT 10

LOCUS R81583 183 bp mRNA EST 12-JUN-1995
YJ0404.r1 Homo sapiens cDNA clone 147727 5' similar to gb:L25119
MU-TYPE OPIOID RECEPTOR (HUMAN);.

ACCESSION R81583
KEYWORDS EST.

SOURCE human clone=147727 library=Soares placenta Nb2HP vector=p7T73D (Pharmacia) with a modified polylinker host=DRI10B (ampicillin resistant) primer=M13RP1 RsiteL=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

AACTGCAAGATTCCGGCGCCGAGCAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 183)

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality.

NCBI gi: 858186

FEATURES

Location/Qualifiers

1..183

/organism="Homo sapiens"

/clone="147727"

/note="human"

BASE COUNT 31 a 56 c 40 g 46 t 10 others

ORIGIN

Query Match 1.9%; Score 27; DB 56; Length 183;

Best Local Similarity 72.7%; Pred. No. 2.31e-11;

Matches 40; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 129 gactggctcgttagtngtggcagattcgtctgctggactccattccat 183

||||| ||||| || ||||| || || ||||| ||||| |||||

QY 1130 GAGTGGCGGTGGTGGTGGCTGCTTTCTGCTGCTGACTCCATACCAT 1184

RESULT 11

LOCUS M78084

DEFINITION EST01672 Homo sapiens cDNA clone HPCPD60 similar to N-formylpeptide

EST 26-MAY-1992

receptor.

ACCESSION M78084

KEYWORDS EST.

SOURCE

human clone=HPCPD60 library=Subtracted Hippocampus, Stratagene (cat. #936205) vector=lamdaZAP-II primer=M13 Forward The hippocampus library (H4 above) was subtracted with a fibroblast cell line cDNA library (Stratagene cat. #936209; W138 lung fibroblast cell line; oligo-dT + random primed cDNA synthesis; lamdaZAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937, 1988).

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 238)

AUTHORS

Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M.,

Uterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.

Sequence identification of 2,375 human brain genes

Nature 355 (6361), 632-634 (1992)

MEDLINE

COMMENT

Contact: Kerlavage AR

The Institute for Genomic Research

932 Clopper Road, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org.

NCBI gi: 273821

Location/Qualifiers

1..238

/organism="Homo sapiens"

/clone="HPCPD60"

/note="human"

<1..>238

/gene="D0S1083E"

BASE COUNT 53 a 70 c 58 g 56 t 1 others

ORIGIN

Query Match 1.9%; Score 28; DB 32; Length 238;

Best Local Similarity 67.5%; Pred. No. 6.32e-13;

Matches 54; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 151 accttgcctcgggtcctgggcaacgggttgatctgctgggtggctggattccggtg 210

||||| ||||| || ||||| ||||| ||||| ||||| |||||

QY 97 ACTTTTTTACTGGGATTGCCAGGCAATGGCTGCTGTGGCTGGCTGAAGATG 156

Db 211 acacacacagtcaccaccat 230

| ||||| | ||| ||

QY 157 CAGCGGACAGTGAACACAT 176

RESULT 12

LOCUS T90501

DEFINITION yel5e04.s1 Homo sapiens cDNA clone 117822 3' similar to gb:M60626

FMET-LEU-PHE RECEPTOR (HUMAN);.

ACCESSION T90501

KEYWORDS EST.

SOURCE human clone=117822 library=Stratagene lung (#937210)

vector=pBluescript SK- host=SOIR cells (kanamycin resistant)

primers=21ml3 RsiteL=EcoRI Rsite2=XhoI Normal lung tissue from a 72

year old male. Cloned unidirectionally. Primer: Oligo dT. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:

5'-GAATTCGCACGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTTT-3'.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E., Waterston, K., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 362
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 719014

FEATURES

Location/Qualifiers

source

1..497

/organism="Homo sapiens"

/clone="117822"

/note="human"

BASE COUNT

119 a 118 c 136 g 120 t 4 others

ORIGIN

Query Match

1.8%; Score 26; DB 86; Length 497;

Best Local Similarity

61.9%; Pred. No. 7.70e-10;

Matches

65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Db 183

tctcgttcaggccctctcaagctggcgggaaggcgtggatcagctctcccggaag 242

Cp 1382

TCCTCACTGAAGGCTGCCTCCAGAAATCCCTGAATGGACTGCCTTCTTCTCTTAA 1323

Db 243

tctggcccatgaagacatagacatgggttgaggcagctnttg 287

Cp 1322

TCTTCCCCAAGGCGCTAAGGAGGATTAACCACTATTG 1278

RESULT 13

LOCUS H29103

249 bp mRNA EST 17-JUL-1995

DEFINITION

Ym31f07.r1 Homo sapiens cDNA clone 49725 5' similar to gb:L06797

PROBABLE G PROTEIN-COUPLED RECEPTOR LCR1 HOMOLOG (HUMAN);.

ACCESSION H29103

KEYWORDS

EST.

SOURCE

human clone=49725 library=Soares infant brain INIB vector=Lafmid BA

host=DH10B (ampicillin resistant) primer=M13R1 Rsite=Not I

Rsite2=Hind III Whole brain from a 73 days post natal female. 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

AACTGAGAAATTCGGCGCCAGCAATTTTTTTTTTTT 3']; double-stranded

cDNA was ligated to Hind III adaptors (Pharmacia), digested with

Not I and directionally cloned into the Not I and Hind III sites of

the Lafmid BA vector. Library went through one round of

normalization. Library constructed by Bento Soares and M.Fatima

Bonaldo.

ORGANISM Homo sapiens

Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 249)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

GDB: G00-422-535
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 198
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 900013

FEATURES

Location/Qualifiers

source

1..249

/organism="Homo sapiens"

/clone="49725"

/note="human"

BASE COUNT

58 a 75 c 55 g 56 t 5 others

ORIGIN

Query Match

1.7%; Score 24; DB 12; Length 249;

Best Local Similarity

60.4%; Pred. No. 6.35e-07;

Matches

64; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Db 104

ggaactgtgaacttgaactctctatgcaggagcagtcctatctatcacacgtcaac 163

Qy 256

GCACAGTGGCCCTACGGCAGGTTCTTATGCAGCTCATCCCTCCATCATTTGCTCAAC 315

Db 164

ctctacagcagtgctctcatcctcctgccttcacagtcctgagccgnt 209

Qy 316

ATGTTTGGCAGTGCTTCTCTGCTTACTGCGATTAGCCTGGATCGCT 361

RESULT 14

LOCUS H14008

198 bp DNA EST 03-JUL-1995

DEFINITION

EST00034 Homo sapiens genomic clone D2-12 5'.

ACCESSION H14008

KEYWORDS

EST.

SOURCE

Human clones=D2-12 library=Chromosome 19p12-p13.1 exon vector=pAMP10

host=E. coli DH5a primer=SD2 : 5' ATC TCA GTG GTA TTT GTC AGC 3'

Exons were isolated from human chromosome 19p12-p13.1 specific

cosmids from Lawrence Livermore National Laboratory using a

modification of the method of exon amplification (Proc. Natl.

Acad. Sci. USA 88: 4005-4009, 1991). Amplified exons were cloned

into pAMP10 by uracil cloning (GIBCOL BRL).

ORGANISM Homo sapiens

Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;



Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed May 1 16:20:37 1996; MasPar time 896.41 Seconds
Tabular output not generated.
1142.027 Million cell updates/sec
Title: >US-08-462-355-1
Description: (1-1446) from US08462355.seq
Perfect Score: 1446
N.A. Sequence: 1 ATGGCGTCTTCTCGTGA.....AAGAAATAGTACACTGTG 1446
Comp: TACCGCAGAAAGAGACGACT.....TTTCTTATCATGTTGACAC

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 264399 seqs, 353985056 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: embl-new11
1-BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN
9:PRI1 10:PRI2 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN
16:UNC 17:VRT 18:VIR
Database: genbank91
19:BCT1 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7
26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAM1 32:MAM2
33:PAT1 34:PAT2 35:PAT3 36:PHG 37:PLN1 38:PLN2 39:PLN3
40:PLN4 41:PLN5 42:PLN6 43:PLN7 44:PRI1 45:PRI2 46:PRI3
47:PRI4 48:PRI5 49:PRI6 50:PRI7 51:PRI8 52:PRI9 53:ROD1
54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR
61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5
68:VRL6 69:VRT1 70:VRT2 71:VRT3
Database: genbank-new11
72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN
79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA
86:VRL 87:VRT
Database: u-embl44 91
88:part1
Statistics: Mean 11.585; Variance 3.952; scale 2.932

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description | Pred. No. |
|------------|-------|-------|--------|----|------------|-----------------------|-----------|
| 1 | 91 | 6.3 | 1080 | 44 | HSC5ANAPL | H.sapiens RNA for rec | 1.02e-67 |
| 2 | 91 | 6.3 | 1092 | 44 | HSC5AR | H.sapiens C5ar rRNA f | 1.02e-67 |
| 3 | 91 | 6.3 | 2328 | 48 | HUMC5AAR | Human C5a anaphylatox | 1.02e-67 |
| 4 | 89 | 6.2 | 1050 | 51 | HUMNEPR | Human N-formylpeptide | 1.73e-65 |
| 5 | 89 | 6.2 | 1281 | 49 | HUMFMPLP26 | Human N-formylpeptide | 1.73e-65 |
| 6 | 89 | 6.2 | 1866 | 49 | HUMFMPLP | Human N-formylpeptide | 1.73e-65 |
| 7 | 89 | 6.2 | 6931 | 49 | HUMFPR1A | Human N-formyl peptid | 1.73e-65 |
| 8 | 88 | 6.1 | 1268 | 32 | RABFPR | Oryctolagus cuniculus | 2.24e-64 |
| 9 | 86 | 5.9 | 1993 | 31 | CFCOMC5AM | C.familiaris mRNA for | 3.71e-62 |
| 10 | 84 | 5.8 | 1058 | 49 | HUMFMPLPX | Human FMLP-related re | 6.03e-60 |
| 11 | 84 | 5.8 | 1650 | 51 | HUMFPR2A | Human formyl peptide | 6.03e-60 |
| 12 | 84 | 5.8 | 1776 | 45 | HSMFPRHO | H.sapiens mRNA for fo | 6.03e-60 |
| 13 | 84 | 5.8 | 1910 | 50 | HUMHM63 | Human mRNA for FMLP-r | 6.03e-60 |
| 14 | 84 | 5.8 | 2631 | 49 | HUMFPR1IA | Human formyl peptide | 6.03e-60 |
| 15 | 76 | 5.3 | 1198 | 49 | HUMFPR12 | Human N-formyl recept | 3.47e-51 |
| 16 | 75 | 5.2 | 1109 | 59 | S50577S2 | C5a anaphylatoxin rec | 4.22e-50 |
| 17 | 75 | 5.2 | 1213 | 55 | MUSC5ACPR | Mus musculus G protei | 4.22e-50 |
| 18 | 72 | 5.0 | 1062 | 49 | HUMFMPLPY | Human RMLP-related re | 7.30e-47 |
| 19 | 73 | 5.0 | 1524 | 57 | MUSNFORREC | Mouse N-formyl peptid | 6.12e-48 |
| 20 | 64 | 4.4 | 1167 | 59 | S74702 | GPRI=G protein-couple | 2.36e-38 |
| 21 | 58 | 4.0 | 1438 | 47 | HSU13666 | Human G protein-coupl | 4.10e-32 |
| 22 | 47 | 3.3 | 1080 | 49 | HUMCR | Homo sapiens chemoatt | 4.29e-21 |
| 23 | 40 | 2.8 | 1583 | 47 | HSU03642 | Human G protein-coupl | 1.82e-14 |
| 24 | 38 | 2.6 | 2051 | 31 | CFGPCR1 | Canis familiaris RDC1 | 1.20e-12 |
| 25 | 38 | 2.6 | 2097 | 10 | HS334481 | Human putative G-prot | 1.20e-12 |
| 26 | 38 | 2.6 | 2097 | 47 | HSU33448 | Human putative G-prot | 1.20e-12 |
| 27 | 36 | 2.5 | 3219 | 59 | RRVTIAIIR | R.rattus mRNA for vas | 7.29e-11 |
| 28 | 36 | 2.5 | 3295 | 57 | RATAT1B | Rat angiotensin recep | 7.29e-11 |
| 29 | 34 | 2.4 | 720 | 59 | S77863 | mu-opioid receptor MO | 4.00e-09 |
| 30 | 35 | 2.4 | 1688 | 59 | S37491 | angiotensin II recept | 5.47e-10 |
| 31 | 33 | 2.3 | 1154 | 47 | HSU17298 | Human kappa opioid re | 2.85e-08 |
| 32 | 33 | 2.3 | 1596 | 9 | HS224911 | Human G protein-coupl | 2.85e-08 |
| 33 | 33 | 2.3 | 1596 | 47 | HSU22491 | Human G protein-coupl | 2.85e-08 |
| 34 | 33 | 2.3 | 1604 | 51 | HUMOPK1B | Homo sapiens (clone d | 2.85e-08 |
| 35 | 32 | 2.2 | 539 | 54 | MMW0R3 | Mus musculus mu opioi | 1.97e-07 |
| 36 | 32 | 2.2 | 1448 | 59 | RNU02083 | Rattus norvegicus mu- | 1.97e-07 |
| 37 | 32 | 2.2 | 1473 | 47 | HSU12569 | Human mu opioid recep | 1.97e-07 |
| 38 | 32 | 2.2 | 1586 | 58 | RATMORA | Rattus norvegicus mu | 1.97e-07 |
| 39 | 32 | 2.2 | 1610 | 82 | MMU26915 | Mus musculus mu opioi | 1.97e-07 |
| 40 | 32 | 2.2 | 1610 | 14 | MM26915 | Mus musculus mu opioi | 1.97e-07 |
| 41 | 32 | 2.2 | 2025 | 47 | HSU07225 | Human P2U nucleotide | 1.97e-07 |
| 42 | 32 | 2.2 | 2025 | 9 | HS07225 | Human P2U nucleotide | 1.97e-07 |
| 43 | 32 | 2.2 | 2135 | 58 | RATMOR1A | Rattus norvegicus Mu | 1.97e-07 |
| 44 | 32 | 2.2 | 2162 | 51 | HUMMOR1X | Human Mu opiate recep | 1.97e-07 |
| 45 | 32 | 2.2 | 2397 | 58 | RATRORB | Rat mRNA for rat opio | 1.97e-07 |

ALIGNMENTS

RESULT 1
LOCUS HSC5ANAPL 1080 bp DNA PRI 02-JUN-1992
DEFINITION H.sapiens RNA for receptor for C5a anaphylatoxin.
ACCESSION X58674
KEYWORDS C5a anaphylatoxin receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

| | | | | | |
|-------------------|---|--|---------|-----|-------------|
| RESULT | 2 | HSC5AR | 1092 bp | PRI | 13-NOV-1992 |
| LOCUS | | H.sapiens C5ar rRNA for C5 anaphylatoxin receptor. | | | |
| DEFINITION | | X57250 | | | |
| ACCESSION | | C5a anaphylatoxin receptor. | | | |
| KEYWORDS | | human. | | | |
| SOURCE | | Homo sapiens | | | |
| ORGANISM | | Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrápoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo. | | | |

| | | |
|----|-----|---|
| | | 405 |
| Db | 346 | atcctgctcaacatgtacgcacgaactcctgtcctgcgcacacatcagcgcgcacgcgttt |
| | | 406 |
| Qy | 304 | ATTGTCCTCAACATCTGTTGGCAGTGTCTCTCTACTTGCACATTAGCCCTAGCATCGCTGT |
| | | 363 |
| Db | 406 | ctgctggtgtttaaacacatcctgggtgcacagaacttcgagggggccggcttggtgcctggatc |
| | | 465 |
| Qy | 364 | CTTGTGTAATCAAGCAACATCTGCTCAGAAATCATCGCAATGTAGGCAATGSCCTGCTCT |
| | | 423 |
| Db | 466 | gcctgtgcgctgctgtggggtttagccctgctgtcgcacacataccctccttctcgtaccgg |
| | | 525 |
| Qy | 424 | ATCTGTGAATGATCTGCGTGGTGGGTTTTGCTGTGCAATCTGCTGTCTGTACCGG |
| | | 483 |

May 1 16:28

US-08-462-355-1.rge

5

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Db 526 g 526
Qy 484 G 484

RESULT 3 HUMC5AAR 2328 bp mRNA PRI 06-MAR-1995
LOCUS Human C5a anaphylatoxin receptor mRNA, complete cds.
DEFINITION M62505 J05327
ACCESSION C5a anaphylatoxin receptor.
KEYWORDS Human peripheral blood promyelocytic leukemia cell line HL-60 (ATCC CCL 240), cDNA to mRNA, clone C5a-receptor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
REFERENCE 1 (bases 1 to 2328)
AUTHORS Boulay,F., Mery,L., Tardif,M., Brouchon,L. and Vignais,P.
TITLE Expression cloning of a receptor for C5a anaphylatoxin on
differentiated HL-60 cells
JOURNAL Biochemistry 30 (12), 2993-2999 (1991)
MEDLINE 91175748
COMMENT NCBI gi: 179699
FEATURES
    Location/Qualifiers
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            /clone="C5a-Receptor"
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                /note="potential translated region; putative; NCBI gi:
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                /translation="MNSFNTPDYGHYDKDLDIATPVDKTSNTLRVPDILALVIF
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                WGLALLTIPSLYRVREYEPKVLGVDYSHDKRRRAVAIVRLVGLFWPLLLT
                TICTYFILLRWSRATRSKTKLVVAVVASFFIFWLPYQVTGIMSFLEPSPPTL
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                polyA_signal
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                    /gene="C5a anaphylatoxin receptor"
BASE COUNT 560 a 645 c 540 g 583 t
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    Query Match 6.3%; Score 91; DB 48; Length 2328;
    Best Local Similarity 60.8%; Pred. No. 1.02e-67;
    Matches 256; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

Db 130 ccagacatcctgcttgatcatttgatcgtctctcctggtggagtgctgggcaat 189
Qy 64 CCAGTAATTCCTCCATTCGCTATTCAGCCTTACTTTTCTACGGATGCCAGGCAAT 123
Db 190 gccctgggtgctgggtgacggatcctcagcgccacgacccatcattgcttcgttc 249
Qy 124 GGGCTGGTCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTTC 183
Db 250 ctcaactggcggtagccgacttctctcctgctgctggcgctgcccatttcttcacgtcc 309
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May 1 16:28

US-08-462-355-1.rge

6

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Qy 244 TTGGCTCTCAGGAGCAGTGGCCCTACGGCAGGTTCTTATGCAAGCTCATCCCTCCATC 303
Db 370 atcctgctcaacatgacccagcatcctgctcctggccacacatcagcgccgacccgcttt 429
Qy 304 ATTGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTTGCATTAGCTGATCGCTGT 363
Db 430 ctgctggtgttaaacccatctggtgccagaacttccagggccgctgtgacctggatc 489
Qy 364 CTTGCTGATTATCAAGCAATCTGCTGTCTCAGAAATCATCGCAATGTAGGGAATGGCCTCT 423
Db 490 gctctgctggctggctgggtttagccctgctgctgacacatcctcctctgctgacgg 549
Qy 424 ATCTGTGATGATCTGCTGGTGGCTTTTGTGTTGCAATTCCTGTCTGCTGCTACCG 483
Db 550 g 550
Qy 484 G 484

RESULT 4 HUMNFR 1050 bp mRNA PRI 02-APR-1991
LOCUS Human N-formylpeptide receptor fMLP-R98 ORF mRNA, 5' end.
ACCESSION M37128
KEYWORDS N-formyl peptide receptor.
SOURCE Human cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
REFERENCE 1 (bases 1 to 1050)
AUTHORS Boulay,F., Tardif,M., Brouchon,L. and Vignais,P.
TITLE Synthesis and use of a novel N-formyl peptide derivative to isolate
a human N-formyl peptide receptor cDNA
JOURNAL Biochem. Biophys. Res. Commun. 168, 1103-1109 (1990)
MEDLINE 90267449
COMMENT NCBI gi: 189183
FEATURES
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                IIRVTVPGKTGTACTNFSPMTNDPKERINAVAMLTVRGIIRFTIGFSAPMSIVA
                VSGLIATKIHKQCLIKSSPPIRLVLSFVAAAFLLQSPYQVVALIATVRIRELQGMV
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BASE COUNT 215 a 300 c 255 g 280 t
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    Query Match 6.2%; Score 89; DB 51; Length 1050;
    Best Local Similarity 63.9%; Pred. No. 1.73e-65;
    Matches 205; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
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| Qy | 97 | ACTTTTTTACTGGGATTGCCAGGCAATGSGGCTGCTGGGTGGCTGCCCTGAAGATG | 156 | | | | | | | |
| Db | 211 | acacacagatcaccaccatcagttacctgaacctggcgctggctgacctgtgtttcaac | 270 | | | | | | | |
| Qy | 157 | CACGGCAGCTGAACAAATTTGGTCTCCACCTCACCTTGGCGGACCTCTCTGCTGC | 216 | | | | | | | |
| Db | 271 | tccactttggccattctcatggtcaggaaaggccatggggagacattggcctttcggtcgg | 330 | | | | | | | |
| Qy | 217 | CTCTCTTTGGGCTCTTCGCTGGGCTCACTTTGGGCTCTCACGGACAGTGGGCGCTACGGCAGG | 276 | | | | | | | |
| Db | 331 | ttcctgtgcaaaattcctctttaccatagtgagacatcaacttgttcgggaagtgattctcctg | 390 | | | | | | | |
| Qy | 277 | TTCTATGCAAGCATCATCCCTCCATCATTTGCTCAACATGTTTTGGCAGTGTCTTCTCTG | 336 | | | | | | | |
| Db | 391 | atgcgcctcattgctctggaccgctgtgttgcgtcctgcattccagctggaccagaac | 450 | | | | | | | |
| Qy | 337 | CTTACTGCCATTAGCTTGAATGCGTGTCTTGTGGTATTCAACCAATCTGGTGTCAGAAT | 396 | | | | | | | |
| Db | 451 | caccgcacgtgagcctggcc | 471 | | | | | | | |
| Qy | 397 | CATCGCAATGTAGGGATGGCC | 417 | | | | | | | |

| | | |
|-------------|--|-----------------------------|
| RESULT | 7 | |
| LOCUS | HUMFPR1A | 6931 bp DNA PRI 18-MAR-1994 |
| DEFINITION | Human N-formyl peptide receptor (FPR1) gene, complete cds and Alu repeats. | |
| ACCESSION | L10820 | |
| KEYWORDS | G protein; G protein coupled receptor; N-formyl peptide; N-formyl peptide receptor; formyl peptide receptor; peptide receptor; pertussis toxin; phagocytosis; plasma membrane; transmembrane domain; transmembrane receptor. | |
| SOURCE | Homo sapiens (Library: Lambda FIX) DNA. | |
| ORGANISM | Homo sapiens | |
| REFERENCE | 1 (sites) | |
| AUTHORS | Boulay,F., Tardif,M., Brouchon,L. and Vignais,P. | |
| TITLE | The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-Protein-Coupled receptors | |
| JOURNAL | Biochemistry 29, 11123-11133 (1990) | |
| MEDLINE | 91105045 | |
| REFERENCE | 2 (sites) | |
| AUTHORS | Perez,H.D. | |
| TITLE | Cloning of the gene coding for a human receptor for formylpeptides | |
| JOURNAL | Unpublished (1992) | |
| REFERENCE | 3 (bases 1 to 6931) | |
| AUTHORS | Murphy,P.M., Tiffany,H.L., McDermott,D. and Ahuja,S.K. | |
| TITLE | Sequence and organization of the human N-formyl peptide receptor-encoding gene | |
| JOURNAL | Gene 133 (2), 285-290 (1993) | |
| COMMENT | 94040825 | |
| FEATURES | NCBI gi: 182739 Location/Qualifiers | |
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VSYGLIAIKTHKGLIKSGRPLRVLSFVAAAFLLCKSPQVVALIATVRIRELQGY
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| ORIGIN | | | |

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| | Best Local Similarity | 63.6%; | Pred. No. 1.73e-65; | | |
| | Matches 205; | Conservative 0; | Mismatches 116; | Indels 0; | Gaps 0; |
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| Qy | 97 | ACTTTTTACTGGGATGGCAGCAATGGCGTGGTCTGGCTGGCTGGCTGCAAGATG | 156 | | |
| Db | 5546 | acacacacagtcaccaccatcagttacctgaactggccctggctgaattctgtttccac | 5605 | | |
| | | | | | |
| Qy | 157 | CAGCGGACAGTGAACAAATTTGGTTCTCTCCACCTCACTTGGCGGACCTCTCTCTGCTGC | 216 | | |
| Db | 5606 | tccactttggcaattcttcattggtcagggaaggccatgggaggaacattggccttttcggctgg | 5665 | | |
| | | | | | |

| | Matches | 216; | Conservative | 0; | Mismatches | 128; | Indels | 0; | Gaps | 0; |
|----|---------|---|--------------|----|------------|------|--------|----|------|----|
| Db | 139 | tctctatttataactcgtcgtcaactttgtcctcggggtctctgggcaacggcgctgggga | 198 | | | | | | | |
| Qy | 74 | TCGCCGTCATTCTCAGCCTTACTTTTTTACTGGATGGCAGCAATGGCGTGGTGC | 133 | | | | | | | |
| Db | 199 | tcctgggtgacgggttcgcgatgactcacacggtcaccacattctctactgaaacctgg | 258 | | | | | | | |
| Qy | 134 | TGTGGGTGGCTGGCCTTGAGATGCAGCGCAGAGTACACAAATTTGGTTCTCTCCACCTCA | 193 | | | | | | | |
| Db | 259 | ccctggcgattctcttcacctccacgctcagctcggttctcattgtcacaaaggccctgg | 318 | | | | | | | |
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254 AGGACAGTGGCCCTGCGCAGGTTCTTATGCAAGCATCATCCCTCCATTTGTCTCA 313
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379 acctgtgggaaggtcttcttgcctcatcgtctggacgcgtgcactgtgtcc 438
Db
314 ACATGTTGGCAGTGTCTTCTCTTACTGCCATTAGCCTGGATCGCTGCTCTTGGTAT 373
Qy
439 tgcaccactctgggccgaaccatcgcaatgaaagctggcc 482
Db
374 TC AAGGCCAATCTGTGTGAGAATCATCGAACTAGGAGATGGCC 417
Qy

| RESULT | 9 | CF5COMC5AM | 1993 bp | RNA | MAM | 30-JUN-1993 |
|------------|---|--|---------|-----|-----|-------------|
| LOCUS | | | | | | |
| DEFINITION | | C.familiaris mRNA for complement C5a receptor. | | | | |
| ACCESSION | | X65860 S52101 | | | | |
| KEYWORDS | | complement protein C5a receptor. | | | | |
| SOURCE | | dog. | | | | |
| ORGANISM | | Canis familiaris | | | | |

| | |
|---|--|
| Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Carnivora; Fissipedia; Canidae; Canis. | |
| 1 (bases 1 to 1993) | |
| Perret, J. | |
| Direct Submission | |
| Submitted (27-APR-1992) to the EMBL/GenBank/DBJ databases. J. | |
| Perret, Université Libre de Bruxelles, I.R.I.B.H.N. ULB Campus Erasme, 808 route de Lennik, 1070 Bruxelles, BELGIUM | |
| 2 (bases 1 to 1993) | |
| Perret, J.J., Raspe, E., Vassart, G. and Parmentier, M. | |
| Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evidence for high interspecies variability | |
| Biochem. J. 288 (Pt 3), 911-917 (1992) | |

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BASE COUNT 405 a 557 c 533 g 498 t
ORIGIN

Query Match 5.9%; Score 86; DB 31; Length 1993;
Best Local Similarity 60.2%; Pred. No. 3.71e-62;
Matches 253; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

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Db 183 ctctcgtggtcgtgggtgacgggtttccagggtccggcgcaaccatcaatgccatcgtgtt 242

Qy 123 TGGCGTGTCTGTGGTGGCTGGCTCGAGATGCGCGGACAGTCAACACAATTTGGTT 182

Db 243 tctcaacgtggcggtggcgagatcctcgtcctcgtcgtggcgtgccatcctgttttcgc 302

Qy 183 CCTCAGCTCAGCTTGGCGGACCTCTCTGCTGCTCTCTTGGCCTTCTGGCTGGCTCA 242

Db 303 catcgtccagcagggtactggcctttggcaacgctcctgcgcgacatcctgcctcgtc 362

Qy 243 CTTGGCTCTCCAGGACAGTGGCCCTACGGCAGGTTCCTATGCAGCTCATCCCTCCAT 302

Db 363 catcgtcacaatgtagccagcatcttgcctgaccacatcagcgccgacgcctt 422

Qy 303 CAFTGTCTCAACATGTTGGCAGTGTCTTCCTGTACTTGCATTTAGCCTGGATCGCTG 362

Db 423 tgccttggtgttaaccatcctggtgccagaactaccgagggcccaagctggcctgggc 482

Qy 363 TCTTGTGTATTCAAGCAATCTGGTGTCAAGATCATCGCAATGTAGGGATGGCCTGCTC 422

Db 483 ggcctgacgctggcctggcgctggcctgctgctgacgtaccctgcgttcattccg 542

Qy 423 TATCTGTGATGTATCTGGGTGGCTGGCTTTTGTGTGTGCAATCTCTGTGTGTGACCG 482

RESULT 10 HUMFLPX 1058 bp mRNA PRI 31-DEC-1994
DEFINITION Human FMLP-related receptor II (FMLP R II) mRNA, complete cds.

ACCESSION M76672
KEYWORDS FMLP-related receptor II; GTP-binding protein;
plasma membrane protein; protein coupled.

SOURCE Homo sapiens (tissue library: human genomic) lung cDNA to mRNA.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1058)
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.

AUTHORS Bao, L., Gerard, N.P., Eddy, R.L. Jr., Shows, T.B. and Gerard, C.
TITLE Mapping of genes for the human C5a receptor (C5AR), human FMLP
receptor (FPR), and two FMLP receptor homolog orphan receptors
(FPRH1, FPRH2) to chromosome 19

JOURNAL Genomics 13 (2), 437-440 (1992)
MEDLINE 92307681

COMMENT NCBI gi: 182666
FEATURES source

Location/Qualifiers
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BASE COUNT 210 a 288 c 255 g 305 t
ORIGIN chromosome 19.

Query Match 5.8%; Score 84; DB 49; Length 1058;
Best Local Similarity 62.1%; Pred. No. 6.03e-60;
Matches 216; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

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Qy 70 ATTCTCTCCATGGTCATCTCAGCCTTACTTTTTTACTGGGATTCGCCAGGCAATGGCGTG 129

Db 139 qtgatctgggtggctgattccggatgacagcagcagtcaccacacatcgttaccctgaac 198

Qy 130 GTGCTGTGGTGGCTGGCCCTGAAGATGACAGCGGACAGTGAACAAATTTGGTTCTCCAC 189

Db 199 ctggcctcgtgctgactttcttcacggccacattaccattcctcattgtctccatggcc 258

Qy 190 CTCACCTTGGCGGACCTCCTCTGCTGCTCTCTTGGCCTTCCTGCGCTGACCTTGGCT 249

Db 259 atggggagaaaatggccttttggctggctcgtgtaagttaattcaatcgcgtggcgac 318

Qy 250 CTCACAGGACGTGGCCCTACGGCAGGCTCTTATGCAAGCTCATCCCTCCATCATTTGTC 309

Db 319 atcaaccttttgaagtgtcttcttgattggtttcaatgcaactggaccgctgatttgt 378

Qy 310 CTCACATGTTGGCAGCTGCTCTCTGCTTACTGCCATTTAGCCTGGATCGCTGCTTGTG 369

Db 379 gtctcgtacccagctcgtggccagacaccacccagctgtgagctcggcc 426

Qy 370 GTATTCAACCAATCTGGTGTGACAAATCATCGCAATGTAGGATGGCC 417

RESULT 11 HUMFPPR2A 1650 bp mRNA PRI 07-JAN-1995
DEFINITION Human formyl peptide receptor (FPR2) mRNA, complete cds.

ACCESSION M88107
KEYWORDS formyl peptide receptor.
SOURCE Homo sapiens (tissue library: lambda-gt11 phage) cDNA to mRNA.

ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.

REFERENCE 1 (bases 1 to 1650)
AUTHORS Ye, R.D., Cavanagh, S.L., Quehenberger, O., Prossnitz, E.R. and
Cochrane, C.G.

TITLE Isolation of a cDNA that encodes a novel granulocyte N-formyl
peptide receptor

JOURNAL Biochem. Biophys. Res. Commun. 184 (2), 582-589 (1992)
MEDLINE 92246937

COMMENT NCBI gi: 189862
FEATURES Location/Qualifiers

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CDS
3'UTR

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Db 118 atctcccatggtggtcgttggtggtcacttctgctcggggtcctgggcaatggcct 177
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Qy 70 ATTCTCTCCATGCTTCTCAGCCTTACTTTTTTACTGGGATTGCCAGCAATGGCGTG 129

Db 178 gtgctcgtggtggctggatccgatgcacagcagtcacacacatctgtacctgaac 237
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Qy 130 GTCTGTGGTGGCTGGCTGAGATGACGCGGACAGTGAACACAATTTGGTTCTCCAC 189

Db 238 ctggccctggtgacttttcttccagggcacattaccattctcattgtctccatggcc 297
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Qy 190 CTCACCTTGGCGGACCTCCTCTGCTGCTCTCTTGGCTTCTGCGCTGCTCCTTGGCT 249

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Qy 250 CTCGAGGACAGTGGCGCTACGGCGAGGTTCCATGCAAGCTCATCCCTCCATCATGTC 309

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Qy 310 CTCACATGTTTGGCAGTGTCTTCTGCTTACTGCCATTAGCCTGCGTGTCTGTG 369

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Qy 370 GTATTCAAGCCAATCTGGTGTGAGATCATGCCAATGATAGGATGGCC 417
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RESULT 12
LOCUS HSEPRHO 1776 bp RNA PRI 05-JUN-1992
DEFINITION H.sapiens mRNA for formyl peptide receptor 70% homologue.
ACCESSION X63819
KEYWORDS formyl peptide receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Cathartini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 1770)
AUTHORS Perez, H.D.
TITLE Cloning of an orphan receptor related to the formyl peptide
receptor of human neutrophils
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1776)
AUTHORS Perez, D.H.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1992) to the EMBL/GenBank/DBJ databases. D.H.
Perez, Berlex Biosciences, 213 E. Grand Ave, South San Francisco,
CA 94080, USA
NCBI gi: 31460
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CDS
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Best Local Similarity 62.1%; Pred. No. 6.03e-60;
Matches 216; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Db 232 atctcccatggtggtcgttggtggtcacttctgctcggggtcctgggcaatggcct 291
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Qy 70 ATTCTCTCCATGCTTCTCAGCCTTACTTTTTTACTGGGATTGCCAGCAATGGCGTG 129

Db 292 gtgactcgtggtggctccgatgcacagcagtcacacacatctgtacctgaac 351
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Db 352 ctggcctcgtgacttttcttccagggcacattaccattctcattgtccatggcc 411
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Qy 190 CTCACCTTGGCGGACCTCCTCTGCTGCTCTCTTGGCTTCTGCTGCTCCTTGGCT 249

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Qy 250 CTCGAGGACAGTGGCGCTACGGCGAGGTTCCATGCAAGCTCATCCCTCCATCATGTC 309

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Qy 310 CTCACATGTTTGGCAGTGTCTTCTGCTTACTGCCATTAGCCTGCGTGTCTGTG 369

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RESULT 13

17-FEB-1994

NCBI q1: 219864

length 1910:

Qv 250 CTCCAGGACAGTGGCCCTACGGCAGGTTCCCTATGCAAGCTCATCCCTCCATCATGTC 309

Db 353 atcaacctcttggagtgctctcttgattggtttcattgcactggaccgctgcatttgt 412

RESULT 14

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

TITLE A structural homologue of the N-formyl peptide receptor.

COMMENT NCBI qi: 182741

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Db 911 gtgactcgggtgggtgagatccggatgacacgcacagtcacacacatctgttacctgaac 970

Qy 130 GTGCTGTGGCTGGCTGGCTGAAGATCAAGATGACGGACAGCAATTTGGTTCCCTCCAC 189

Db 971 ctggccctggctgacttttcttccagggccacatcaccattccattctctccatggcc 1030

Qy 190 CTCACCTTGGCGGACCTCCTCTGCTGCTCTCCTTGGCTTCTGCTGGCTCACTTGGCT 249

Db 1031 atgggagaaaatggccttttggctgttctctgtgaagttaattcaatcactgtgtggac 1090

Qy 250 CTCACGGCAGTGGCTTACGGCAGGTCTCTATGCAAGCTCATCCCTCCATCATTTGC 309

Db 1091 atcaacctttggaagtgtcttcttgatgtttcattgtcactggacgctgcatttgt 1150

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Qy 370 GTATTCAAGCCAATCTGCTGTCTCAGAAATCATCGCAATGTAGGGATGGCC 417

RESULT 15 HUMFRL2 1198 bp DNA PRI 08-NOV-1994

LOCUS Human N-formyl receptor-like 2 protein (FRL2) gene, complete cds.

ACCESSION L14061

KEYWORDS N-formyl peptide receptor-like 2 protein; transmembrane protein.

SOURCE Homo sapiens (tissue library: lambda FIX; Stratagene) adult DNA.

ORGANISM Homo sapiens

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homiidae.

REFERENCE 1 (bases 1 to 1198)

AUTHORS Durstin,M., Gao,J.L., McDermott,D. and Murphy,P.M.

TITLE Structural and functional analysis of the human N-formyl peptide receptor gene cluster

JOURNAL Unpublished (1993)

COMMENT NCBI gi: 292034

FEATURES

source

CDS

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/note="NCBI gi: 292035"

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BASE COUNT 280 a 301 c 264 g 353 t

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Best Local Similarity 61.5%; Pred. No. 3.47e-51;

Matches 203; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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Qy 134 TGTGGTGGCTGGCTGAAGATGCGACGGACAGTGAACACAATTTGGTTCTCTCCACCTCA 193

Db 282 ccttagctgaacttcttcttcagtgccatcctaccattccgaatggctcagtcgccatga 341

Qy 194 CCTTGGCGGACCTCTCTGCTGCCCTCTCCTTGGCTTCTGCGTGCCTCACTTGGCTCTCC 253

Db 342 gagaaaaatggccttttggctcattctcatgtaagttagttcatgttatgatagacatca 401

Qy 254 AGGCACAGTGGCCCTAGCGCAGGTTCCTATGCAGAGCTCATCCCTCCATCATTTCTCTCA 313

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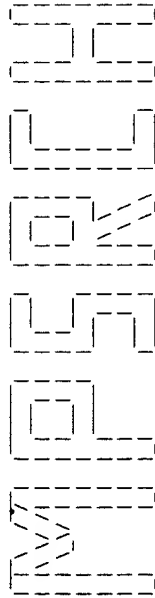
Qy 314 ACATGTTTGGCAGTGTCTTCTCTGCTTACTGCCATTAGCCTGCATCGCTGTCTTGTGGTAT 373

Db 462 tgcataccagcctgggcccagaacccatcgca 491

Qy 374 TCAGGCCAATCTGGTGTCTCAGAATCATCGCA 403

Search completed: Wed May 1 16:35:48 1996

Job time : 911 secs.



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 1 16:36:07 1996; MasPar time 111.87 Seconds
859.505 Million cell updates/sec

Tabular output not generated.

Title: >US-08-462-355-1
Description: (1-1446) from US08462355.1
Perfect Score: 1446
N.A. Sequence:
Comp: 1 ATGCGCTTTCTCTGCTGA.....AAAGAAATAGTACAACTGTG 1446
TACCGCAGAAAGACGACT.....TTTCTTATCATGTTGACAC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 84802 seqs, 33246950 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq22

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 9.408; Variance 5.327; scale 1.766

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
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| c 1 | 85 | 5.9 | 1047 | 2 | Q10572 Human Natriuretic Pep 1.63e-39 | |
| 2 | 62 | 4.3 | 1047 | 2 | Q10572 Human Natriuretic Pep 5.41e-24 | |
| c 3 | 47 | 3.3 | 204 | 1 | N81164 Base substituted E.co 2.42e-14 | |
| c 4 | 43 | 3.0 | 91 | 9 | Q51746 Oligonucleotide probe 7.19e-12 | |
| 5 | 42 | 2.9 | 91 | 9 | Q51746 Oligonucleotide probe 2.93e-11 | |
| 6 | 41 | 2.8 | 204 | 1 | N81164 Base substituted E.co 1.18e-10 | |
| 7 | 40 | 2.8 | 1872 | 11 | Q66176 Seven transmembrane r 4.74e-10 | |
| 8 | 38 | 2.6 | 2098 | 11 | Q66177 Seven transmembrane r 7.38e-09 | |
| 9 | 34 | 2.4 | 114 | 12 | Q70469 Generic DNA sequence 1.57e-06 | |

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| 10 | 34 | 2.4 | 114 | 12 | Q70465 | Generic DNA sequence | 1.57e-06 |
| 11 | 34 | 2.4 | 114 | 12 | Q70470 | Generic DNA sequence | 1.57e-06 |
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| 16 | 34 | 2.4 | 720 | 11 | Q66173 | Seven transmembrane r | 1.57e-06 |
| c 17 | 33 | 2.3 | 114 | 12 | Q70467 | Generic DNA sequence | 5.83e-06 |
| 18 | 33 | 2.3 | 1000 | 13 | Q75931 | Human kappa opioid re | 5.83e-06 |
| 19 | 33 | 2.3 | 1054 | 15 | Q83681 | Epsilon opioid recept | 5.83e-06 |
| c 20 | 32 | 2.2 | 114 | 12 | Q70466 | Generic DNA sequence | 2.13e-05 |
| 21 | 32 | 2.2 | 114 | 12 | Q70468 | Generic DNA sequence | 2.13e-05 |
| 22 | 32 | 2.2 | 829 | 10 | Q56703 | Partial sequence of t | 2.13e-05 |
| 23 | 32 | 2.2 | 1610 | 15 | Q89226 | Human mu opioid recep | 2.13e-05 |
| 24 | 32 | 2.2 | 1618 | 15 | Q89223 | Transcription regulat | 2.13e-05 |
| 25 | 32 | 2.2 | 1618 | 15 | Q89222 | Rat mu opioid recepto | 2.13e-05 |
| 26 | 32 | 2.2 | 1842 | 15 | Q88134 | Human P20 receptor ge | 2.13e-05 |
| 27 | 32 | 2.2 | 1981 | 10 | Q56705 | Partial sequence of t | 2.13e-05 |
| 28 | 32 | 2.2 | 2070 | 12 | Q79199 | Rat mu-subtype opioid | 2.13e-05 |
| 29 | 32 | 2.2 | 2160 | 15 | Q93102 | Human mu opiate recep | 2.13e-05 |
| 30 | 32 | 2.2 | 3871 | 2 | N71302 | HSV-1 gB and surround | 2.13e-05 |
| 31 | 30 | 2.1 | 114 | 12 | Q70472 | Generic DNA sequence | 2.73e-04 |
| c 32 | 31 | 2.1 | 114 | 12 | Q70466 | Generic DNA sequence | 7.68e-05 |
| c 33 | 31 | 2.1 | 114 | 12 | Q70470 | Generic DNA sequence | 7.68e-05 |
| 34 | 29 | 2.0 | 114 | 12 | Q70471 | Generic DNA sequence | 9.52e-04 |
| 35 | 29 | 2.0 | 120 | 11 | Q66150 | Seven transmembrane r | 9.52e-04 |
| c 36 | 28 | 1.9 | 114 | 12 | Q70472 | Generic DNA sequence | 3.26e-03 |
| c 37 | 27 | 1.9 | 498 | 3 | N50034 | Sequence encoding new | 1.10e-02 |
| c 38 | 27 | 1.9 | 501 | 3 | N50031 | Sequence encoding new | 1.10e-02 |
| c 39 | 27 | 1.9 | 501 | 3 | N50032 | Sequence encoding new | 1.10e-02 |
| c 40 | 27 | 1.9 | 501 | 3 | N50027 | Sequence encoding new | 1.10e-02 |
| c 41 | 27 | 1.9 | 501 | 3 | N50033 | Sequence encoding new | 1.10e-02 |
| c 42 | 27 | 1.9 | 501 | 3 | N50028 | Sequence encoding new | 1.10e-02 |
| c 43 | 27 | 1.9 | 501 | 3 | N50023 | Sequence encoding new | 1.10e-02 |
| c 44 | 28 | 1.9 | 1567 | 15 | Q89233 | Rat opioid receptor c | 3.26e-03 |
| 45 | 28 | 1.9 | 2706 | 16 | Q92972 | Rat opiorph receptor | 3.26e-03 |

ALIGNMENTS

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| ID | Q10572; standard; DNA; 1047 BP. |
| AC | Q10572; |
| DT | 09-APR-1991 (first entry) |
| DE | Human Natriuretic Peptide Receptor B. |
| KW | NPBR; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; |
| KW | hyperaldosteronism; glaucoma; guanyl cyclase. |
| OS | Homo sapiens. |
| FH | Key |
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| FT | /label= cytoplasmic domain |
| FT | /note= "GC and protien kinase activity" |
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| FT | Modified -site 35..37 |

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FT Modified -site 600..602
FT /label= N-glycos site
PN W09100292-A.
PD 10-JAN-1991.
PF 22-JUN-1990; 003586.
PR 23-JUN-1989; US-370673.
PA (GETH ) GENENTECH INC.
PI Chang M, Goeddel D, Lowe D;
DR WPI; 91-036711/05.
DR N-PSDB; Q10324.
PT Natriuretic protein receptor B - for diagnosis and treatment of
PT kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
PS Claim 3; Fig 1; 49pp; English.
CC The sequence was derived from the DNA encoding natriuretic peptide
CC receptor B, NPRB, having guanyl cyclase (GC) activity and protein
CC kinase activity. The DNA can be inserted into expression vectors
CC for the prodn. of the protein, opt. after being mutated to produce
CC NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=
CC 114,952). The protein (or variants) can be used in treatment of
CC natriuretic peptide disorders, and also to isolate peptides using
CC affinity chromatography. Antibodies with affinity for NPRB can
CC also be prepd.
SQ Sequence 1047 BP; 87 A; 15 C; 83 G; 51 T;

Query Match 5.9%; Score 85; DB 2; Length 1047;
Best Local Similarity 9.0%; Pred. No. 1.63e-39;
Matches 88; Conservative 279; Mismatches 597; Indels 12; Gaps 12;

Db 29 vnnnnhnsyavawrvgnavanavanngrannvdrnrvssnnngacsnynannsaavdnk 88
Cp 1228 CCAGGGAGTTTCGGTCAAGCAATGACAGGACTCCCAAAATGTGTATGGAGTCC 1169

Db 89 nyhdndnnngvcvynaasvarnasahwrnnmntagavasgsakndhyrtnvrtgnsank 148
Cp 1168 AGCAGACAGAAAGACAGCCACCACCCAGCGGCTCGAAAGGTTTGTCTGAGACT 1109

Db 149 ngnnvvttnhghnnwtarannnyndatddrhnhytnngvnnannsgnsvnhnvyarng 208
Cp 1108 TGGCGAAGCGCCCTTCAT-TCGGAGACAATGAAGCTGTAACAGGCTATCATGATA 1050

Db 209 gnnnathnrangrnrvncggnnmhnnhnnnannrnnntngdyvnnndvngnsragnt 268
Cp 1049 ACAGAGGCGACGAGAAACCCACCTAGCTGATGCTGCTAT-T-CCACAGCGGGTG 992

Db 269 atgrwndntrnnanannamntvntyrnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 328
Cp 991 TTGGCACTTGATCGTCACTGTGAATGGCCTAAATGTGAATTCCTGGAACCTTGTG 932

Db 329 nannnagcnydgpnnyavnnntnnngtrndgrnrvnkngrryhgvtgngvmdkndr 388
Cp 931 GTAGCT-CAGACTCGTAGAAGGAATTCGTAGAAGCGCTAGGGAACAGCTTTAAATGATGA 873

Db 389 ntshvnmangdnsgdnnaahysganknwrtgrnnnnvkvgnnsdnnncandndhsc 448
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Db 449 dkttnethav-angtntnnmgvsennnrkmmnnknnasnnwrrnrvnnnnngnery 507
Cp 813 ACTGGGGATTTTGTGTCAGACCACATCAGCAGGTTTAAATACATTAGATACA-GATT-T 756
Db 508 hkgagrsntnsrsgssygsmtahgkynnntghnkgnvvvankhvknnrntnrvnnn 567
Cp 755 TGACTTGTTAACCTAGCAGAACCCCTAGGAGTGAATCTGCA-GAAGGTCTTTGAATGT 697
Db 568 nkhrdvnnhntnmgacndnnnncvntnycnrgsnndnnnnndnnndnnnnndnn 627
Cp 696 TTGAGGTTGGAAGACAGCTGGGACCTGTCAGAGCATCATTTGTTGGAAGAGGAAGG 637
Db 628 vkmmnnhnsnshsgnsksncvvdvsnrvnknktdygnasnrstannddnnanyaknnt 687
Cp 636 ATCTAACCTATCATTTCTTCTCAGGGCGCTGAACAATGTTTCAAGAGACCTGTTTC 577
Db 688 annnnegnnnttgmaaadvyngnnnnnnnnnnnnnnnnngnngndnsknkvrvngnry 747
Cp 576 TAGTGGATCCCATAAAGTCTGGATAATCTAATGAGCTGAGAGACCAAAATTTGTAGCC 517
Db 748 nrnsndrtnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 807
Cp 516 ACATCTATTATGTTGTCGTAGTCAAGATTTCCCGGTACAGACACAGGAAATGCACAA 457
Db 808 yannnnknnvntnnyannnnkrkanannnnnnnnnnnnnnnnnnnnnnnnnnnnnn 867
Cp 456 CACAAA-AGCCACCCACCCAGATACATCCACAGATAGACAGGCGCATCCCTACATTCGAT 398
Db 868 vyntansanstmmvvtvnnndnytcndannndndvykvtntngdaymvvsgnngnngnriha 927
Cp 397 GATTCTGA-CACAGATTTGGCTTGAATACCACAAAGACAGCGCATCCAGGCTAATGGCAGTA 339

Db 928 nnarmanannndavsnrrhrhndnnrnnngvhtgncvagvgnkmmrvnngdvtnta 987
Cp 338 AGCAGGAAGACACTGCCAAACATGTTGAGGACAATG-ATGGAGGGCGATGAGCTTGCATAG 280

Db 988 srmsngnankhvas 1003
Cp 279 GAACCTCCCGTAGGCC 264

RESULT 2
ID Q10572 standard; DNA; 1047 BP.
AC Q10572;
DT 09-APR-1991 (first entry)
DE Human Natriuretic Peptide Receptor B.
KW NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
KW hyperaldosteronism; glaucoma; guanyl cyclase.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= signal sequence
FT Protein 12
FT /label= mature NPRB
FT Domain 23..455
FT /label= extracellular domain
FT /note= "binds natriuretic peptides A, B and C"
FT Domain 456..456
FT /label= transmembrane domain
FT Domain 479..1047
FT /label= cytoplasmic domain
```


CC and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q0466-68. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.

Sequence 114 BP: 0 A; 2 G; 2 G; 2 T;

[illegible]

| | | |
|--------|--|------------------------|
| RESULT | 13 | |
| ID | Q70468 | standard; DNA; 114 BP. |
| AC | Q70468; | |
| DT | 05-APR-1995 | (first entry) |
| DE | Generic DNA sequence to generate a random TSAR petide library. | |
| KW | TSAR; totally synthetic affinity reagent; synthetic; binding domain; | |
| KW | effector domain; concatenated heterofunctional protein; linker; | |
| KW | direct; rapid; detection; screening; treatment; generic; as. | |
| OS | Synthetic. | |
| FH | Key | Location/Qualifiers |
| FT | misc feature | 55..60 |
| FT | /*tag= a | |
| FT | /note= *this sequence represents 'Z'; Z can be a | |
| FT | sequence of 6, 9 or 12 nucleotides (see | |
| FT | comments)* | |
| PN | W09418318-A. | |
| PD | 18-AUG-1994. | |
| PF | 01-FEB-1994; U000977. | |
| PR | 01-FEB-1993; US-013416. | |
| PR | 30-DEC-1993; US-176500. | |
| PR | 31-JAN-1994; US-189331. | |
| PA | (UYNC-) UNIV NORTH CAROLINA. | |
| PI | Fowlkes DM, Kay BK; | |
| PI | WPI; 94-279739/34. | |
| DR | P-FSDB; R65154. | |
| PT | Identifying proteins or peptide(s) which bind a ligand - by | |
| PT | screening a recombinant vector library expressing fusion proteins | |
| PT | comprising a binding domain and an effector domain | |
| PS | Disclosure; Page 35; 255pp; English. | |
| CC | Q70468 is a generic DNA sequence used to generate random TSAR (Totally | |

PS Disclosure; Page 35; 255pp; English.

1

Search completed: Wed May 1 16:38:05 1996
Job time : 118 secs.

(T)

Release 2.1D John F. Collins, BioComputing Research Unit.
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```

MPsrch_pp  protein - protein database search, using Smith-Waterman algorithm

Run on:      Wed May 1 15:29:30 1996;  MasPar time 19.61 Seconds
           621.257 Million cell updates/sec

Tabular output not generated.

```

```

Title:
Description:
Perfect Score:
Sequence:

```

Scoring table: PAM 150
Gap 11

Searched: 82306 segs. 25270970 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:
pir46
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1
13:unrev2
```

Statistics: Mean 48.219: Variance 119.102: scale 0.405

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description | Pred. No. |
|------------|-------|-------|--------|----|--------|----------------------|-----------|
| | | Match | Length | | | | |
| 1 | 601 | 16.7 | 352 | 11 | S27357 | complement C5a recep | 1.01e-73 |
| 2 | 580 | 16.2 | 350 | 10 | A37963 | complement C5a anaph | 2.58e-70 |
| 3 | 579 | 16.1 | 351 | 10 | B42009 | FMPL-related recepto | 3.74e-70 |
| 4 | 555 | 15.5 | 351 | 11 | A45525 | C5a anaphylatoxin re | 2.84e-66 |
| 5 | 553 | 15.4 | 353 | 10 | C42009 | FMPL-related recepto | 5.98e-66 |
| 6 | 536 | 14.9 | 364 | 11 | A49542 | N-formyl peptide che | 3.28e-63 |
| 7 | 525 | 14.6 | 352 | 11 | A46520 | N-formyl peptide rec | 1.92e-61 |
| 8 | 521 | 14.5 | 350 | 10 | A42009 | N-formyl peptide rec | 8.44e-61 |
| 9 | 439 | 12.2 | 353 | 11 | JC2492 | G protein-coupled re | 9.42e-48 |
| 10 | 419 | 11.7 | 355 | 10 | A55733 | G protein-coupled re | 1.31e-44 |
| 11 | 369 | 10.3 | 362 | 10 | JN0694 | angiotensin II recep | 7.84e-37 |
| 12 | 360 | 10.0 | 359 | 13 | S44425 | angiotensin II recep | 1.90e-35 |

| | | | | | | |
|----|-----|------|--------|--------|----------------------|----------|
| 13 | 360 | 10.0 | 359 11 | JC1194 | angiotensin II recep | 1.90e-33 |
| 14 | 357 | 9.9 | 359 11 | A4C114 | type-1 angiotensin I | 5.50e-35 |
| 15 | 357 | 9.9 | 359 10 | JC1104 | angiotensin II recep | 5.50e-35 |
| 16 | 356 | 9.9 | 359 13 | S15403 | angiotensin II recep | 7.83e-35 |
| 17 | 355 | 9.9 | 359 11 | AQ0578 | angiotensin II recep | 1.11e-34 |
| 18 | 352 | 9.8 | 359 11 | A4Z656 | angiotensin II recep | 1.21e-34 |
| 19 | 352 | 9.8 | 359 13 | S20423 | angiotensin II recep | 3.21e-34 |
| 20 | 350 | 9.7 | 359 11 | A4B857 | AT1 angiotensin II r | 6.50e-34 |
| 21 | 346 | 9.6 | 359 11 | JH0622 | angiotensin receptor | 2.66e-33 |
| 22 | 340 | 9.5 | 352 10 | A53103 | leukocyte-derived se | 2.19e-32 |
| 23 | 340 | 9.5 | 352 11 | A45747 | receptor D2S201E - h | 2.19e-32 |
| 24 | 340 | 9.5 | 352 10 | S32761 | neuropeptide Y recep | 2.19e-32 |
| 25 | 341 | 9.5 | 359 11 | JQ1516 | angiotensin II recep | 1.54e-32 |
| 26 | 338 | 9.4 | 359 11 | JC2134 | angiotensin II recep | 4.41e-32 |
| 27 | 338 | 9.4 | 359 11 | JH0621 | angiotensin receptor | 4.41e-32 |
| 28 | 338 | 9.4 | 359 13 | S20424 | angiotensin II recep | 4.41e-32 |
| 29 | 338 | 9.4 | 359 13 | S15404 | Angiotensin II recep | 4.41e-32 |
| 30 | 335 | 9.3 | 355 10 | A53611 | interleukin-8 recept | 1.26e-31 |
| 31 | 335 | 9.3 | 355 10 | A39446 | interleukin-8 recept | 1.26e-31 |
| 32 | 332 | 9.2 | 353 11 | S28787 | neuropeptide Y recep | 3.60e-31 |
| 33 | 331 | 9.2 | 355 11 | JQ1231 | interleukin-8 recept | 5.11e-31 |
| 34 | 332 | 9.2 | 359 11 | JC1193 | angiotensin II recep | 3.60e-31 |
| 35 | 325 | 9.1 | 350 10 | A39445 | interleukin-8 recept | 4.14e-30 |
| 36 | 328 | 9.1 | 359 11 | JQ1055 | angiotensin II recep | 1.46e-30 |
| 37 | 324 | 9.0 | 353 10 | A53858 | bradykinin receptor | 5.87e-30 |
| 38 | 321 | 8.9 | 238 10 | PN0449 | angiotensin II recep | 1.67e-29 |
| 39 | 315 | 8.8 | 248 11 | A46226 | somatostatin recepto | 1.34e-28 |
| 40 | 315 | 8.8 | 418 13 | S32501 | somatostatin recepto | 1.34e-28 |
| 41 | 312 | 8.7 | 428 11 | S30508 | probable G protein-c | 3.78e-28 |
| 42 | 311 | 8.7 | 428 11 | A44021 | somatostatin recepto | 5.35e-28 |
| 43 | 306 | 8.5 | 398 13 | S34593 | opioid receptor - ra | 3.01e-27 |
| 44 | 305 | 8.5 | 400 13 | S41075 | mu opiate receptor - | 4.24e-27 |
| 45 | 296 | 8.2 | 354 11 | A21669 | interleukin-8 recept | 9.36e-26 |

ALIGNMENTS

| | |
|------------|---|
| RESULT | 1 |
| ENTRY | S27357 |
| TITLE | #type complete complement C5a receptor - dog |
| ORGANISM | #formal_name Canis lupus familiaris #common_name dog |
| DATE | 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995 |
| ACCESSIONS | S27357 |
| REFERENCE | S27357 |
| #authors | Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M. |
| #journal | Biochem. J. (1992) 288:911-917 |
| #title | Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evidence for high interspecies variability. |

[illegible]

| | | |
|-------------------|---|--|
| Db | 77 | lnlavaddlscialpilfssivqgypfgnaacrllpslllmmysaillltisadrf 136 |
| Qy | 62 | lhltladiLCCLSLAFSLAHALQCGMPYGRFLCKLIPSIIVLNFGSVFLTAISLDR 121 |
| Db | 137 | lvfnlpiwcnvrgpqdlawaacsavavallltvpsifrgvht 180 |
| Qy | 122 | lvvfkptwcnhrnrvnvmacsicgcitwvavfvlciptvfyreift 165 |
| RESULT | 2 | |
| ENTRY | A37963 | #type complete |
| TITLE | | complement C5a anaphylatoxin receptor - human |
| ORGANISM | | #formal name Homo sapiens #common name man |
| DATE | 22-Jan-1993 | #sequence_revision 22-Jan-1993 #text_change |
| | 28-Oct-1994 | |
| ACCESSIONS | A37963; S13646; S30518 | |
| REFERENCE | A37963 | |
| #authors | Boulay, F.; Mery, L.; Tardif, M.; Brouchon, L.; Vignaia, P. | |
| #journal | Biochemistry (1991) 30:2993-2999 | |
| #title | Expression cloning of a receptor for C5a anaphylatoxin on differentiated HL-60 cells. | |
| #cross-references | MUID:911175748 | |
| #accession | A37963 | |
| | #molecule type mRNA | |
| | #residues 1-350 | #label B0U |
| | #cross-references | GB:J05327 |
| REFERENCE | S13646 | |
| #authors | Gerard, N.P.; Gerard, C. | |
| #journal | Nature (1991) 349:614-617 | |
| #title | The chemotactic receptor for human C5a anaphylatoxin. | |
| #cross-references | MUID:91156029 | |
| #accession | S13646 | |
| | #status preliminary | |
| | #molecule type mRNA | |
| | #residues 1-350 | #label GER |
| KEYWORDS | G protein-coupled receptor; glycoprotein; membrane protein | |
| FEATURE | 5 | |
| | #binding site carbohydrate (Asn) (covalent) #status predicted | |
| SUMMARY | #length 350 #molecular-weight 39320 #checksum 3557 | |
| | Query Match 16.2%; Score 580; DB 10; Length 350; | |
| | Best Local Similarity 47.2%; Pred. No. 2,586-70; | |
| | Matches 67; Conservative 45; Mismatches 30; Indels 0; Gaps 0 | |
| Db | 36 | pdilaalvifavflvgvlgmalvwtvtafeakrtinaiflnlavadflscialpilfts 95 |
| Qy | 22 | pvlshvllstlftlglpngvlvavaglkvortvnttwtflhtladlccLSLAFSLAH 81 |
| Db | 96 | ivqthhhwpfgaacilpslllmmysaillltisadrfllvfkptwcnvrgaglawi 155 |
| Qy | 82 | lvaqcmvpygrfLCKLIPSIIVLNFGSVFLTAISLDRCLVFKPTWCNHRNVMACS 141 |
| Db | 156 | acawawglallltipsflyrvv 177 |
| Qy | 142 | icgcitwvavfvlciptvfyrei 163 |
| RESULT | 3 | |
| ENTRY | B42009 | #type complete |
| TITLE | | FMPL-related receptor 1 - human |
| ALTERNATE_NAMES | FMPL receptor homolog FPR2; formyl peptide receptor like-1; probable chemotactic receptor FPRH1 | |
| ORGANISM | #formal name Homo sapiens #common name man | |

| DATE | 30-Sep-1993 | sequence_revision | 14-Jul-1995 | text_change | |
|-----------------------|---|-------------------|-------------------|------------------|---------------|
| ACCESSION | B42009; | JC1258; | JQ1521; | A42492; | S21581 |
| REFERENCE | A42009 | | | | |
| authors | Bao, L.; Gerard, N.P.; | Eddy Jr., R.L.; | Shows, T.B.; | Gerard, C. | |
| # journal | Genomics (1992) | 13:437-440 | | | |
| # title | Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), and two FMLP receptor homologue orphan receptors (FPRH1, FPRH2) to chromosome 19. | | | | |
| # accession | B42009 | | | | |
| ##molecule_type | DNA | | | | |
| ##residues | 1-263, | 'A', 265-338, | 'C', 340-351 | ##label | BAO |
| ##cross-references | GB:M76672 | | | | |
| ##note | nucleotide sequence is not given; authors translated the codons GTC for residue 15 as Glu, TCT for residue 19 as Thr, and GGC for residues 264 as Ala; translation for residue 265 was not shown | | | | |
| REFERENCE | JC1258 | | | | |
| authors | Perez, H.D.; | Holmes, R.; | Kelly, E.; | McClary, J.; | Andrews, W.H. |
| # journal | Gene (1992) | 118:303-304 | | | |
| # title | Cloning of a cDNA encoding a receptor related to the formyl peptide receptor of human neutrophils. | | | | |
| #cross-references | MUID:92380523 | | | | |
| # accession | JC1258 | | | | |
| ##molecule_type | mRNA | | | | |
| ##residues | 1-351 | ##label | PER | | |
| ##cross-references | EMBL:X63819 | | | | |
| ##experimental_source | bone marrow mRNA | | | | |
| ##note | nucleotide sequence is not given | | | | |
| REFERENCE | JQ1521 | | | | |
| authors | Ye, R.D.; | Cavanagh, S.L.; | Quehenberger, O.; | Prossnitz, E.R.; | |
| # journal | Cochrane, C.G. | | | | |
| # title | Biochem. Biophys. Res. Commun. (1992) | 184:582-589 | | | |
| #cross-references | MUID:92246937 | | | | |
| # accession | JQ1521 | | | | |
| ##molecule_type | mRNA | | | | |
| ##residues | 1-351 | ##label | YE2 | | |
| ##cross-references | GB:M88107 | | | | |
| ##experimental_source | granulocytes | | | | |
| ##note | formyl peptide-stimulated calcium mobilization compatible to that of the formyl peptide receptor is seen at 1000 times higher concentrations of ligand | | | | |
| | Met-Leu-Phe | | | | |
| REFERENCE | A42492 | | | | |
| authors | Murphy, P.M.; | Ozcelik, T.; | Kenney, R.T.; | Tiffany, H.L.; | |
| # journal | McDermott, D.; | Frankie, U. | | | |
| # title | J. Biol. Chem. (1992) | 267:7637-7643 | | | |
| #cross-references | NCBI:94159; | NCBIP:94160 | | | |
| ##note | A structural homologue of the N-formyl peptide receptor. Characterization and chromosome mapping of a peptide chemoattractant receptor family. | | | | |
| #cross-references | MUID:92218423 | | | | |
| # accession | A42492 | | | | |
| ##molecule_type | mRNA | | | | |
| ##residues | 1-351 | ##label | MUR | | |
| ##cross-references | NCBI:94159; | NCBIP:94160 | | | |
| ##note | sequence extracted from NCBI backbone | | | | |
| COMMENT | This G-protein coupled receptor, homologous to the N-formyl peptide receptor FPR1, does not bind prototype N-formyl peptide ligands (reference A42492, but see also JQ1521). It is expressed only on differentiated myeloid cells and is probably a chemotactic | | | | |

receptor for some other ligand.

GENETICS

gene GDB:FPRL1

#map position 19q13.3-q13.4

#introns #status absent

chemotaxis response; G protein-coupled receptor;
glycoprotein; transmembrane protein

KEYWORDS

FEATURE

27-53 #domain transmembrane #status predicted #label TR1\

59-83 #domain transmembrane #status predicted #label TR1\

100-121 #domain transmembrane #status predicted #label TR1\

145-169 #domain transmembrane #status predicted #label TR1\

206-226 #domain transmembrane #status predicted #label TR1\

242-266 #domain transmembrane #status predicted #label TR1\

282-307 #domain transmembrane #status predicted #label TR1\

4 #binding site carbohydrate (Aen) (covalent) #status predicted\

```

98-176      #disulfide_bonds #status predicted
SUMMARY    #length 351 #molecular-weight 38964 #checksum 3402

```

Query Match 16.1%; Score 579; DB 10; Length 351;
Best Local Similarity 46.5%; Pred. No. 3.74e-70;
Matches 72; Conservative 43; Mismatches 39; Indels 1; Gaps 1;

D6

27 ilplwlvgtfvlvgvlgnglviwwagfrmtvttycynlaladfstatlplflvsma 86
|||:::||::||: |||::||||: || | |:|:|||| :||: :::

Qy 24 ILSWILSIFLLGLPGNGLVFWAGIKMQRTVNTIWFHLTLADLLCCLSLAFSLAHLA 83

| | | | | | | | | | | |
|------|----|----------------|-----------|----------|--------|--------|---------|---------|------------------|-----|
| D6 | 87 | mgeawpfgwflckl | ihlvvdnlf | gsvfl | lgfial | drcicv | lhpvwag | hrtvs | lankvi | 146 |
| | | : | : : | ::: : | : | : : : | : : : : | : : : : | : : : : | |
| A... | 94 | laccawvcdpfcv | ldeyiv | nmecsvti | lta | lci | ndc | lwtckd | lfcawhduwvawcsic | 143 |

04 LQGGMF IGRF EOKLLP31V LMTF G3VF E5TAT3ZLWACBVFNF IROQWIKUWGTAC31C 147

D6 147 YGpw:la|v|t|p|v|f|f|t|t|v|t|p|n|g|d|t|v|c|t|f|n|f|a 181

Qy 144 GCIAWVAFVLCIPVFVYREIFTTDNNHR-CGYKFG 177

| | |
|------------|--|
| RESULT | 4 |
| ENTRY | |
| TITLE | A46525 #type complete
C5a anaphylatoxin receptor, C5aε-peptidergic
G-protein-coupled receptor - mouse |
| ORGANISM | #formal name Mus musculus #common name house mouse |
| DATE | 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
28-Apr-1995 |
| ACCESSIONS | A46525 |
| REFERENCE | A46525 |
| #authors | Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.;
Gerard, N.P. |
| #journal | J. Immunol. (1992) 149:2600-2606 |
| #title | Structural diversity in the extracellular faces of
peptidergic G-protein-coupled receptors. Molecular cloning
of the mouse C5a anaphylatoxin receptor. |

#cross-references MUID:93017861

```

#accession A46525
##status preliminary; not compared with conceptual translation
##molecule type nucleic acid

```

```
##molecule_type nucleic acid
##residues 1-351 ##label GER
```

##cross-references NCBIP:116075
##experimental source PAIP/C

```
##experimental_source path/c
##note      sequence extracted
```

SUMMARY #length 351 #molecula

Query Match 15.5%; Score 555; DB 11; Length 351;

Best Local Similarity 42.9%; Pred. No. 2.84e-66;

Matches 70; Conservative 46; Mismatches 45; Indels 2; Gaps 1;

```
Db 31 pkrqgdvaaliiysvflvgpgnalvwvtafedpgpsnaiwflnlavadllslamp 90
| : | : : : : | : : : | : : : : : : : | : : : : : | : : : : : | : : : : : |
```

Qy 17 PNNEPVILSWILSLTFLGLCPGNGILWVAGIKMQRTVNTWFLHLTLADLLCCLSIA 76

```

Db      91 v|fttv|n|n|w|y|f|d|a|c|i|v|p|s|i|l|n|m|y|a|s|i|l|l|a|t|i|s|a|d|r|f|i|l|v|k|p|w|c|q|k|v|r|g|t|
      150
Qw      77 f|s|i|a|h|i|n|o|c|a|d|y|c|b|e|t|c|i|t|p|s|i|l|v|n|w|e|c|s|v|i|t|a|i|s|i|p|r|c|i|n|w|e|k|r|w|c|o|h|r|n|v|
      136

```

151 qlawmacgawvialliltipsfvyreavkdfysehtvcqinyv 193

Qy 137 GMACSGCIWVAFVLCIPVYVREIFTT--DHNRCGYKFG 177

| | |
|-----------------|--|
| RESULT | 5 |
| ENTRY | |
| TITLE | C42009 #type complete |
| ALTERNATE_NAMES | FM1P-related receptor 2 - human |
| ORGANISM | FM1P-related receptor 1; probable chemotactic receptor FPRH2 |
| DATE | formal name Homo sapiens common name man |
| | 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change |
| | 14-Jul-1995 |

ACCESSIONS
C42009
REFERENCE
A42009

#authors
C.
C.
C.

Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard,
C. 1 41000 12 437 440

| # | Journal | Genomics (1992) 13:431-440 | Mapping of genes for the human C5a receptor (C5AR), human EMIP receptor (FPR) and two EMIP receptor homologous orphan |
|---|---------|----------------------------|---|
| 1 | Journal | Genomics (1992) 13:431-440 | Mapping of genes for the human C5a receptor (C5AR), human EMIP receptor (FPR) and two EMIP receptor homologous orphan |

#accession C42009

```
##molecule_type DNA
##residues 1-353 ##label BAO
```

##cross-references GB:M/6673
##note nucleotide sequence is not given

COMMENT This met-leu-pne receptor homolog, whose ligand is not yet known, appears not to be expressed in neutrophils.

GENETICS

```
# gene      GDB:FPRL2
#map position 19q13.3-q13.4
```

#introns
#status absent
chemotaxis response; G protein-coupled receptor;
KEYWORDS

SUMMARY
glycoprotein; transmembrane protein
#length 353 #molecular-weight 40015 #checksum 8135

Query Match 15.4%; Score 553; DB 10; Length 353;
Best Local Similarity 40.0%; Pred. No. 5.98e-66;

Matches 72; Conservative 56; Mismatches 49; Indels 3; Gaps 3;

```
Db      3 tnfslplneteevlpaghtvlwfslvhgvtfvfgvlgnglvwagfmrtrvtntl 62
```

Qy 2 ASFSAEITNSID-LISQPMNEPPV-IISMVILSLTFELASLPGNGGLVLMVAGLEKQRTIVNTI 59

ph 63 culalaladcfcaailofemvuvamrkmfaeflaklulumididilfvrnulititild 122

DD CYNHARCAUSISALPRIMVSAMERXPPASICKIVMNVSVYVETIACAD IZ
QV WEHLTADLLCCSLAFSAHLAGOWPYGRFLCKLPSIIIVANEGGSVELTAISLD I19

Db 123 rci cvlhpaw aqh rhtnslak rvm tglw ifrvi ltpn fiftt istng dty cifnfaf 182

QY
120 RCLVFEKPIWCQNHRNVGMACISCGCIWVAVFLCIPVFVYRE-IFTTNDNHRCGYKEGL 178

| | | |
|--------|--------|----------------|
| RESULT | 0 | |
| ENTRY | A49542 | #type complete |

| | | | |
|-----------------------|---|--|--|
| TITLE | N-formyl peptide chemotactic receptor - mouse | | |
| ORGANISM | #formal_name Mus musculus #common_name house mouse | | |
| DATE | 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 23-Mar-1995 | | |
| ACCESSIONS | A49542 | | |
| REFERENCE | A49542 | | |
| authors | Gao, J.L.; Murphy, P.M. | | |
| #journal | J. Biol. Chem. (1993) 268:25395-25401 | | |
| #title | Species and subtype variants of the N-formyl peptide chemotactic receptor reveal multiple important functional domains. | | |
| #accession | A49542 | | |
| #status | preliminary | | |
| #molecule_type | DNA | | |
| #residues | 1-364 #label GAO | | |
| #cross-references | GB:L22181 | | |
| GENETICS | | | |
| #introns | #status absent | | |
| KEYWORDS | chemotaxis; transmembrane protein | | |
| SUMMARY | #length 364 #molecular-weight 40326 #checksum 3042 | | |
| Query Match | 14.9%; Score 536; DB 11; Length 364; | | |
| Best Local Similarity | 43.4%; Pred. No. 3,28e-63; | | |
| Matches | 75; Conservative 54; Mismatches 38; Indels 6; Gaps 6 | | |
| Db | 35 vfsyliavftvlgvnglvieagfmrkhtvtisylvnlaiadf-ctfstlpfyiasm 93 | | |
| Qy | 24 ILSWILSLTFLGLPGNGLVIMVAGIKMQRTVNTLHLTLADLCLCS-LAFSLAHL 82 | | |
| Db | 94 vmgghwpfwmckfiyvtvidinlfgsvfllialldrcicvlhvwagmhrtvelakvv 153 | | |
| Qy | 83 ALQGGWPYGRFLKLPISITVILNMFSGVFLTAISLDRCILVWFKQIWQNHRRNVGMACSI 142 | | |
| Db | 154 iivpwicaflltlpvil-r-l-ttvpnsrlg-pgktactdfsfptkdpvekr 202 | | |
| Qy | 143 CGCIWVAFVLCIPFVYVREITFDTHNRCKYKFGLSLSDYDFYGDPLENR 195 | | |
| RESULT | 7 | | |
| ENTRY | A46520 #type complete | | |
| TITLE | N-formyl peptide receptor - rabbit | | |
| ORGANISM | #formal_name Oryctolagus cuniculus #common_name domestic rabbit | | |
| DATE | 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995 | | |
| ACCESSIONS | A46520 | | |
| REFERENCE | A46520 | | |
| authors | Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prossnitz, E.R.; Cochran, C.G. | | |
| #journal | J. Immunol. (1993) 150:1383-1394 | | |
| #title | The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and structure/function implications. | | |
| #cross-references | MUID:93163563 | | |
| #accession | A46520 | | |
| #status | preliminary; not compared with conceptual translation | | |
| #molecule_type | nucleic acid | | |
| #residues | 1-352 #label YE1 | | |
| #cross-references | NCBI:P124908 | | |
| #experimental_source | NZM, neutrophils | | |
| #note | sequence extracted from NCBI backbone | | |
| SUMMARY | #length 352 #molecular-weight 38674 #checksum 7066 | | |
| Query Match | 14.6%; Score 525; DB 11; Length 352; | | |
| Best Local Similarity | 47.3%; Pred. No. 1.92e-61; | | |

[illegible]

15

QY 80 AHIALQGQWPYGRFLCKLIPSIIVLNMFGSVFLLTAISLDRCLVVFKEPIMCQNHNRVGM 139

tciiwllaglaslpaihrnvvffientnltvcafhyesqns1191

ICGCIWWAFVLCIPVFVYREIFTTDNHN-R-CGYKF-GLSSSL 182

Search completed: Wed May 1 15:30:45 1996
Job time : 75 secs.

| | |
|----|--|
| PI | Godiska R, Gray PW, Schweickart VL; |
| DR | WPI; 94-200264/24. |
| DR | N-PSDB; Q66177. |
| DR | DNA encoding seven trans:membrane receptors - used to develop |
| PT | prods. for use as therapeutic or diagnostic agents for conditions |
| PT | involving the receptors. |
| PT | Example 10; Page 77-78; 100pp; English. |
| PS | PCR using two primers (Q66174, Q66175) was performed to amplify a |
| CC | partial sequence of the R20 seven transmembrane coding sequence |
| CC | which was later used as a probe for isolating the R20 genomic clone |
| CC | (Q66176) from a human placenta DNA library. During the isolation |
| CC | of the R20 gene, two weakly hybridising sequences were identified |
| CC | which had significant homology to other seven transmembrane |
| CC | receptors. The probe was used to screen a human genomic foetal |
| CC | liver DNA library, and while the R20 gene could not be identified in |
| CC | this library, several weakly hybridising clones were plaque |
| CC | purified, subcloned and sequenced. The two clones were designated |
| CC | R2 and R12 (Q66178). This is the sequence encoded by the R2 clone. |
| SQ | Sequence 377 AA; |

| | | | | |
|-----------------------|--------|--|----------------|-------------------|
| Query Match | 10.9%; | Score 390; | DB 10; | Length 377; |
| Best Local Similarity | 40.4%; | Pred. No. 7.17e-24; | | |
| Matches | 57; | Conservative 42; | Mismatches 40; | Indels 2; Gaps 2; |
| Db | 44 | llaillavallavlgpnsfvswsilkrmqkrsvtalmvlnlaladlavlltapffhlhfl | 103 | |
| Qy | 24 | llswwllslltflglpncglvllwaglkwq-rvntwfwfhlhladllccslasfslahl | 82 | |
| Db | 104 | a-dgtwsglagrcrlchyycgvswyavslitamsldrslavarpfvsqklrtkamarv | 162 | |
| Qy | 83 | alqogmpygrfclklipslivnmgsvflltalsldrcrlwfkpfcwcnhrnvgmacti | 142 | |
| Db | 163 | lagiwlvsflllatpvlavrtv | 183 | |
| Qy | 143 | cgciwvafvflcipvfvvreyi | 163 | |

| RESULT | 2 |
|--------|--|
| ID | R44531 standard; Protein; 359 AA. |
| AC | R44531; |
| DT | 24-JUN-1994 (first entry) |
| DE | Human angiotensin II type 1 receptor. |
| KE | Angiotensin; Ang II; receptor; antagonist; hypertension. |
| KW | Homo sapiens. |

| Key | Location/Qualifiers |
|-----|----------------------------------|
| FT | 187..313 |
| FT | Protein |
| FT | /note="claim 1" |
| PN | CA2093495-A. |
| PD | 08-OCT-1993. |
| PF | 06-APR-1993; 093495.. |
| PF | 07-APR-1992; JP-085445. |
| PR | 21-APR-1992; JP-101393. |
| PR | 17-FEB-1993; JP-027835. |
| PA | (TAKE) TAKEDA CHEM LTD. |
| PI | Fujisawa Y, Konishi H, Kuroda S; |
| DR | WFI; 94-000128/01. |
| DR | N-PDSB; 053486. |

PT Human angiotensin II type 1 receptor polypeptide useful for
PT determining human angiotensin II type 1 receptor antagonist
PT activity
PT Claim 2; Fig 1; 42pp; English.
PS Human Ang II type 1 receptor is useful for determining the
CC bioactivity of angiotensin II type 1 receptor antagonists which are
CC useful for treating hypertension. The Ang II type 1 receptor gene
CC

[illegible]

| RESULT | 3 |
|--------|---|
| ID | R53753 standard; Protein; 337 AA. |
| AC | R53753; |
| DT | 07-FEB-1995 (first entry) |
| DE | Seven transmembrane receptor (RM3). |
| DE | Seven transmembrane receptor; receptor; amplification; PCR; |
| KW | primer; seven transmembrane receptor; receptor; amplification; PCR; |
| KW | polymerase chain reaction. |

| OS | Key | Location/Qualifiers |
|----|---------|-----------------------|
| FT | Domain | 48..69 |
| FT | /label= | Transmembrane domain. |
| FT | Domain | 82..100 |
| FT | /label= | Transmembrane domain. |
| FT | Domain | 115..136 |
| FT | /label= | Transmembrane domain. |
| FT | Domain | 159..179 |
| FT | /label= | Transmembrane domain. |
| FT | Domain | 198..220 |
| FT | /label= | Transmembrane domain. |
| FT | Domain | 246..274 |
| FT | /label= | Transmembrane domain. |
| FT | Domain | 287..311 |
| FT | /label= | Transmembrane domain. |

PN W09412635-A.
PD 09-JUN-1994.
PE 17-NOV-1993; U11153.
PF 17-NOV-1993; U11153.
PG 17-NOV-1992; US-977452.
PH (ICOS-) ICOS CORP.
PI Godiska R, Gray PM, Schweickart VL;
PJ WPI; 94-200264/24.
PK N-PSDB; Q66179.
PL DNA encoding seven trans:membrane receptors - used to develop
PM prods. for use as therapeutic or diagnostic agents for conditions
PN involving the receptors.
PO Example 11; Page 84-85; 100pp; English.
PP Two primers (Q66148, Q66149) were used in a PCR reaction containing
PQ human macrophage cDNA library in plasmid pRC/CMV. When the PCR
PR products were subjected to agarose gel electrophoresis a faint band
PS of 180-200 base pairs was observed. Re-amplified material was
PT digested with BamHI and HindIII and cloned into the plasmid
PU Bluescript SK-. Of sixteen clones sequenced, two contained a unique
PV sequence termed RM3. Specific primers for the partial RM3 clone were
PW used to identify a full length RM3 cDNA clone (Q66179) which

CC encoded this seven transmembrane receptor.
SQ Sequence 337 AA;

| | | | | |
|-----------------------|--|---------------------|----------------|-------------------|
| Query Match | 9.5%; | Score 340; | DB 10; | Length 337; |
| Best Local Similarity | 34.2%; | Pred. No. 2.00e-19; | | |
| Matches | 53; | Conservative 42; | Mismatches 55; | Indels 5; Gaps 5; |
| Db | 24 iflp-ttysiiftgtvgnglvilvmgydkkrlremtdkyzllhlsvadllfvitlpfwavid 82 | | | |
| | ::: ::: | ::: | ::: | |
| Qy | 23 VILSWVILLSLTFLLGTPGNGLVIWVACL-KMORTVTNTFLHTLTADLLCCLSLAFSLAH 81 | | | |
| Db | 83 -av-anwygfnickavhyvtvnyssvlllafisdrylaivhatnsqrpkllaekv 140 | | | |
| | : : : : : : : : : : : : | | | |
| Qy | 82 LALQGOWPYGREKULPSIVITVMNFGSVFLTAISDRCLVWFPRTWCONHRNVGMACS 141 | | | |
| Db | 141 vvygwipallltltpdifanvseadryicd-rf 174 | | | |
| | : : : : : : : : : : : : : : : : : : : | | | |
| Qy | 142 ICGGTIVWVAFLGIPVEFYREIFTTDNNHRCYKF 176 | | | |

RESULT

| | |
|----|---|
| ID | R68812 standard; Protein; 352 AA. |
| AC | R68812; |
| AD | 18-JUL-1995 (first entry) |
| DE | Human monocyte PF4AR. |
| KW | Interleukin-8 receptor; IL-8 receptor; PF4AR; |
| KW | platelet factor superfamily receptor; monocyte; chemotactic; |
| KW | inflammation; inflammatory disease; arthritis; emphysema; cystic; |
| KW | fibrosis; colitis; bronchitis; meningitis; therapeutic. |
| OS | Homo sapiens. |
| PN | W09428931-A. |
| PD | 22-DEC-1994. |
| PF | 07-JUN-1994; U06380.. |
| PR | 11-JUN-1993; US-076093. |
| PA | (GETH) GENENTECH INC. |
| PI | Chuntharapai A, Hebert C, Kim KJ, Lee J; |
| DR | WPI; 95-036114/05. |
| NR | N-PSDB; Q80521. |
| PT | Treatment of inflammatory disorders - by administering an |
| PT | antibody capable of binding a platelet factor 4 superfamily |
| PT | receptor polypeptide |
| PS | Disclosure; Page 54-56; 83pp; English. |
| CC | 2 PF4AR members were identified by probing lambda libraries from |
| CC | human monocyte-like cell line HL-60 and human peripheral blood |
| CC | lymphocytes using a large fragment of IL-8 receptor DNA (full |
| CC | sequence given in Q80520). The nucleotide sequences of the 2 |
| CC | PF4ARs are given in Q80521 and Q80522, and their respective |
| CC | amino acid sequences in R68812 and R68813. |
| SQ | Sequence 352 AA; |

| | | | | |
|-----------------------|--------|--|----------------|-------------------|
| Query Match | 9.5%; | Score 340; | DB 12; | Length 352; |
| Best Local Similarity | 34.2%; | Pred. No. 2.00e-19; | | |
| Matches | 53; | Conservative 42; | Mismatches 55; | Indels 5; Gaps 5; |
| Db | 39 | iflp-tiyeiifltigvngqlvlvmgyqkkrstmkryrlhlsvadllfvitlpfwavd | 97 | |
| Qy | 23 | viilsfllstfllgicpgnlwvagi-kmqrvtnttflhltdlclclslafslah | 81 | |
| Db | 98 | -av-anwfgnlckavhviytnvlysefllafisdrylaivhatnsgrprkllaev | 155 | |
| Qy | 82 | lalgompygrfclcklpsiiivnmfsgsvelltaisdrcldwvfrpfcwqnhrrvmgacs | 141 | |
| Db | 156 | vyvgwvpaallltipdfifanvseadryicd-rf | 189 | |

QV 142 ICGIWWAFVLCIPVFVYREIFTTDHNRCCYKF 176

| | | |
|--------|--|--|
| RESULT | 5 | |
| ID | R27792 standard; Protein; 352 AA. | |
| AC | R27792; | |
| AD | AC | |
| DE | 12-MAR-1993 (first entry) | |
| DT | New platelet factor 4 receptor superfamily member PF4ARI. | |
| KW | IL-8R; G-protein coupled receptor family; rhodopsin superfamily; | |
| KW | pro-inflammatory cytokine; 8rr.20.15. | |
| OS | Homo sapiens. | |
| PN | W09217497-A. | |
| PD | 15-OCT-1992. | |
| PF | 23-MAR-1992; U02317. | |
| PR | 29-MAR-1991; US-677211. | |
| PR | 19-DEC-1991; US-810782. | |
| PA | (GETH) GENENTECH INC. | |
| PI | Holmes WE, Lee J, Wood WI; | |
| WI | WPI; 92-366191/44. | |
| DR | N-PSDB; Q29506. | |
| PT | Isolated human platelet factor 4 super-family receptor | |
| PT | polypeptide and corresp. antibodies and DNA - useful as | |
| PT | diagnostic and screening agents, and for treating inflammation o | |
| PT | PF4AR-mediated disorders | |
| PS | Claim 7; Fig 4; 78pp; English. | |
| CC | The IL-8 receptor cDNA sequence was isolated (see Q29505) and a | |
| CC | 874bp sub-fragment of the coding sequence was used as a probe to | |
| CC | screen human cell line HL60 and human peripheral blood lymphocyte | |
| CC | cDNA libraries. Two new gene sequences were found that are clearly | |
| CC | related to the IL-8 receptor. One of these was contained in | |
| CC | combined clone 8rr.20.15 and is predicted to encode an amino aci | |
| CC | sequence which is 34% identical with both the high and low affin | |
| CC | IL-8 receptors. See also Q37107. | |
| CC | Sequence 352 AA; | |

| | | | | |
|-----------------------|--------|---------------------|--------|----------------|
| Query Match | 9.5%; | Score 340; | DB 5; | Length 352; |
| Best Local Similarity | 34.2%; | Pred. No. 2.00e-19; | | |
| Matches | 53; | Conservative | 42; | Mismatches 55; |
| | | | Indels | 5; |
| | | | Gaps | 5; |

[illegible]

RESULT

| | |
|----|---|
| ID | R33420 standard; Protein; 355 AA. |
| AC | R33420; |
| DT | 26-JUL-1993 (first entry) |
| DE | Human IL-8 receptor from clone p2. |
| KW | Interleukin-8 receptor; probes; gene therapy; gro receptor; |
| KW | intracellular-calcium mobilising; ligand-binding; MIP-2 receptor. |
| OS | Homo sapiens. |
| PN | W09306229-A. |
| PD | 01-APR-1993. |
| PF | 14-SEP-1992; U07641. |
| PR | 13-SEP-1991; US-759568. |

(USSH) US DEPT HEALTH & HUMAN SERVICE.
Murphy PM;
WPI; 93-117549/14.
N-PSDB; Q38747.
New interleukin-8 receptor aminoacid sequence - and corresp. cDNA
expressed in Xenopus laevis oocytes or transfected host cells,
for screening ligands of IL-8 receptor and gene therapy
Claim 1; Fig 3; 39pp; English.
cDNA libraries from 2 and 3.5 kb fractions of poly(A) + RNA from HL60
neutrophils sepd. of a sucrose gradient were made in UniZAP[®]. The
libraries were screened with F3R oligonucleotide probe (from rabbit
IL-8 receptor) and under low stringency with a p2 cDNA probe
synthesised from random primers, to isolated the clone p2, encoding
human IL-8 receptor protein. The presence or absence of the DNA
encoding IL-8R or related MIP-2 receptor may be detected using
portions of the p2 clone as probes. P2 may also be used to screen
for ligands of IL-8R and may also be used in gene therapy to treat a
patient deficient in IL-8R. The IL-8R is a gto receptor and has
intracellular calcium-mobilising and ligand-binding properties.
Sequence 355 AA;
SO

[illegible]

| | | |
|--------|---|-----------------------------------|
| RESULT | 7 | |
| AC | AD | R28273 standard; Protein; 360 AA. |
| AD | AC | R28273; |
| DT | 04-APR-1993 | (first entry) |
| DE | Sequence in a low affinity recombinant human interleukin-8 | |
| DE | (IL-8) receptor polypeptide in 4AB. | |
| DE | IL-8 receptor polypeptide; G-protein-coupled receptor. | |
| KW | Homo sapiens. | |
| OS | | |
| PN | W09218641-A. | |
| PP | 29-OCT-1992. | |
| PF | 10-APR-1992; U02977. | |
| PR | 10-APR-1991; US-685101. | |
| PR | 09-JUL-1991; US-726006. | |
| PR | 09-DEC-1991; US-803842. | |
| PA | (REPK) REPLIGEN CORP. | |
| PA | (UYBO-) UNIV BOSTON. | |
| PI | Navarro J, Thomas KM, Witt DP; | |
| DR | WPI; 92-382123/46. | |
| DR | N-PSDB; Q30012. | |
| PT | Recombinant mammalian interleukin-8 receptor - used for screening | |
| PT | interleukin-8 binding antagonists, used to treat inflammation | |
| PST | Disclosure; Fig 2; 71pp; English. | |
| CC | Rabbit high affinity IL-8 receptor gene was isolated from rabbit | |
| CC | peritoneal neutrophils and used as a source of poly(A) + RNA, to | |
| CC | produce a rabbit neutrophil cDNA library. 250,000 recombinant | |
| CC | plagues were screened for those which hybridized to an antisense | |

oligonucleotide (Q30015). This probe was designed based on the sequence derived from the second transmembrane domain of G-protein-coupled receptors. After tertiary screening, six plaques were isolated. The insert of one of these plaques, termed F3R was of 2.5 kb in size. This insert was sequenced. The protein deduced from the F3R clone demonstrates that it belongs to the family of G-protein-coupled receptors. The deduced protein sequence indicates seven putative transmembrane segments. A human peripheral blood leukocyte lambda gt10 cDNA library (5' stretch) was screened with a 652 bp EcoRI/BamHI fragment (including nucleotides -21 to 625) of the rabbit F3R clone. After tertiary screening several human clones which hybridized to the rabbit IL-8 probe were isolated. The insert of one such clone, termed 4AB was sequenced (Q30012).

[illegible]

| | | |
|--------|--|--|
| RESULT | 8 | |
| ID | R70124 standard; Protein; 1064 AA. | |
| AC | R70124; | |
| DT | 14-FEB-1996 (first entry) | |
| DE | I18-R type 2-GSP 130 fusion protein. | |
| KW | Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; | |
| KW | red blood cell; cytokine receptor; glycophorin binding peptide 130; | |
| KW | GSP 130; GSPH; glycophorin binding peptide homologue; glycophorin A. | |
| OS | Chimeric Homo sapiens. | |
| OS | Chimeric Plasmodium falciparum. | |
| PN | W09506737-A. | |
| PD | 09-MAR-1995. | |
| PF | 01-SEP-1994; G01900. | |
| PR | 03-SEP-1993; GB-018350. | |
| PR | 23-AUG-1994; GB-017021. | |
| PA | (PREN/) PRENDERGAST K F. | |
| PI | Prendergast KF; | |
| DR | WPI; 95-115452/15. | |
| PT | New hybrid peptide(s) for binding cytokine(s) - comprising a | |
| PT | malaria parasite peptide capable of binding a red blood cell and | |
| PT | a receptor peptide. | |
| PS | Example A; Page 80-82; 93pp; English. | |
| CC | Hybrid peptides for binding cytokines, comprising a malaria parasite | |
| CC | (Plasmodium falciparum) peptide (capable of binding to a red blood | |
| CC | cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples | |
| CC | of these hybrid peptides. R70124 is a fusion of interleukin 8 receptor | |
| CC | type 2 and glycophorin binding protein (GSP) 130. The use of cytokine | |
| CC | receptors not normally found on RBCs means that the cytokine can bind | |
| CC | harmlessly to the RBC without deleterious effect. The RBC protects the | |
| CC | hybrid peptides from excretion from the kidney, and due to steric | |
| CC | hindrance prevents the cytokines binding to a receptor in another cell. | |

CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC PMSA (pre major merozoite surface antigen) and the Duffy binding
CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on
CC the surface of RBCs. The hybrid peptides are thus used to lower
CC the levels of free cytokines in the circulation to reduce pathological
CC damage.
SQ Sequence 1064 AA;

Query Match 9.34; Score 335; DB 14; Length 1064;

Best Local Similarity 32.0%; Pred. No. 5.53e-19;

Matches 48; Conservative 49; Mismatches 47; Indels 6; Gaps 6;

Db 46 viiyalvlllqslgmvlvylsvrsvtdvllnlaladllfaltlpiwaas-kvn 104

Qy 27 MWLSLFLGLPGNGVLVWAGL-KMQRTVNTWFLHLTLADLCCLSIAFLAHALQ 85

Db 105 q-wifgtfclkvslkvevfysgilllaciavdrylaivhatrtltqkry-lvkfcils 162

Qy 86 QMPYGRFLCKLIPSIIVINMGVSFLTLAISLDRCLVWFKPIWQCNHRNVGMACSGCG 145

Db 163 iwgllalllpvllfrtvyssnvspac-y 191

Qy 146 IWWAFVLCIPFVYR-EIFTTDNHRGCG 174

RESULT 9

ID R28272 standard; Protein; 355 AA.

AC R28272;

DT 04-APR-1993 (first entry)

DE Sequence in a high affinity recombinant rabbit interleukin-8

DE (IL-8) receptor polypeptide in F3R.

KW IL-8 receptor polypeptide; G-protein-coupled receptor.

OS Oryctolagus cuniculus.

PN W09218641-A.

PD 29-OCT-1992.

PF 10-APR-1992; U02977.

PR 10-APR-1991; US-685101.

PR 09-JUL-1991; US-726606.

PR 09-DEC-1991; US-803842.

PA (REPK) REPLIGEN CORP.

PA (UYBO-) UNIV BOSTON.

PI Navarro J, Thomas KM, Witt DP;

DR WPI; 92-382123/46.

DR N-PSDB; Q30011.

PT Recombinant mammalian interleukin-8 receptor - used for screening

PT interleukin-8 binding antagonists, used to treat inflammation

PS Claim 2; Fig 1; 71pp; English.

CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit

CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to

CC produce a rabbit neutrophil cDNA library. 250,000 recombinant

CC plaques were screened for those which hybridized to an antisense

CC oligonucleotide (Q30015). This probe was designed based on the

CC sequence derived from the second transmembrane domain of G-protein-

CC coupled receptors. After tertiary screening, six plaques were

CC isolated. The insert of one of these plaques, termed F3R was of 2.5

CC kb in size. This insert was sequenced. The protein deduced from

CC the F3R clone demonstrates that it belongs to the family of

CC G-protein-coupled receptors. The deduced protein sequence

CC indicates seven putative transmembrane segments.

SQ Sequence 355 AA;

Query Match

9.24; Score 331; DB 6; Length 355;

Best Local Similarity 30.9%; Pred. No. 1.25e-18;
Matches 46; Conservative 50; Mismatches 49; Indels 4; Gaps 4;

Db 48 viiyalvlllqslgmvlvylsvrsvtdvllnlamadllfaltlpiw-a-vske 105

Qy 27 MWLSLFLGLPGNGVLVWAGL-KMQRTVNTWFLHLTLADLCCLSIAFLAHALQ 85

Db 106 kwifgtfclkvslkvevfysgilllaciavdrylaivhatrtltqkrh-lvkfcilg 164

Qy 86 QMPYGRFLCKLIPSIIVINMGVSFLTLAISLDRCLVWFKPIWQCNHRNVGMACSGCG 145

Db 165 iwalslilslpfflfrqvfspnspvcy 193

Qy 146 IWWAFVLCIPFVYR-EIFTTDNHRGCG 174

RESULT 10

ID R27791 standard; Protein; 350 AA.

AC R27791;

DT 12-MAR-1993 (first entry)

DE Interleukin-8 receptor.

KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;

KW pro-inflammatory cytokine.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 40..67

FT /label= transmembrane

FT /note= "putative"

FT Domain 76..98

FT /label= transmembrane

FT /note= "putative"

FT Domain 112..133

FT /label= transmembrane

FT /note= "putative"

FT Domain 155..174

FT /label= transmembrane

FT /note= "putative"

FT Domain 204..226

FT /label= transmembrane

FT /note= "putative"

FT Domain 243..264

FT /label= transmembrane

FT /note= "putative"

FT Domain 292..312

FT /label= transmembrane

FT /note= "putative"

PN W09217497-A.

PD 15-OCT-1992.

PF 23-MAR-1992; U02317.

PR 29-MAR-1991; US-677211.

PR 19-DEC-1991; US-810782.

PA (GETH) GENENTECH INC.

PI Holmes WE, Lee J, Wood WI;

DR WPI; 92-366191/44.

DR N-PSDB; Q29505.

PT Isolated human platelet factor 4 super-family receptor

PT polypeptide and corresp. antibodies and DNA - useful as

PT diagnostic and screening agents, and for treating inflammation or

PT PF4AR-mediated disorders

PS Claim 7; Fig 2; 78pp; English.

CC A cDNA library constructed from human neutrophil mRNA in the mammalian

CC expression vector pRK5B was transfected into COS-7 cells as pools of

CC 2500 clones. One positive pool from the first 58 transfections was

CC partitioned into smaller pools until a pure clone (pRK5B.i18r1.1)

CC was obtained. The ORF encodes a protein of 350 amino acids which shares several features with the G-protein coupled receptors of the rhodopsin superfamily, including 7 hydrophobic (transmembrane) domains. The IL-8 receptor is a preferred PF4AR superfamily member of the invention. See also Q29506 and Q37107.

SQ Sequence 350 AA;

Query Match 9.1%; Score 325; DB 5; Length 350;
Best Local Similarity 31.3%; Pred. No. 4.21e-18;
Matches 47; Conservative 46; Mismatches 51; Indels 6; Gaps 6;

Db 43 iiayalvfllslgslmvlvlysvrsvtdvylnlaladllfaltlpiaaas-kvm 101

Qy 27 MWLSLTFLLGLPGNGLVWVAGL-KMORTVNTWFLHLTLADLLCCLSLAFSLAHIAIQ 85

Db 102 g-wifgtfclkvsvllkevnfygilllacisvdrylaivhatrtltqkth-lvkfvcqlg 159

Qy 86 GQMPYGRFLCKLIPSIIVLNMGFSVFLTAISLDRCLWFKP IWCQNHRNVGMCSIC-G 144

Db 160 c-wglamslpfflfrqayhpnnsqvcy 188

Qy 145 CIWVAFVLCIPVFVYREIFTTDDHNRGCGY 174

RESULT 11

ID R68811 standard; Protein; 350 AA.

AC R68811;

DT 18-JUL-1995 (first entry)

DE Interleukin-8 receptor.

KW Interleukin-8 receptor; IL-8 receptor; PF4AR;

KW platelet factor superfamily receptor; neutrophil; chemotactic;

KW inflammation; inflammatory disease; arthritis; emphysema; cystic;

KW fibrosis; colitis; bronchitis; meningitis; therapeutic.

OS Homo sapiens.

PN W09428931-A.

PD 22-DEC-1994.

PF 07-JUN-1994; U06380.

PR 11-JUN-1993; US-076093.

PA (GETH) GENENTECH INC.

PI Chuncharapai A, Hebert C, Kim KJ, Lee J;

DR WPI; 95-036114/05.

DR N-PSDB; Q80520.

DR Treatment of inflammatory disorders - by administering an

PT antibody capable of binding a platelet factor 4 superfamily

PS receptor polypeptide

PS Disclosure; Page 51-54; 83pp; English.

CC A cDNA library constructed from human neutrophil mRNA in pRKS5B was

CC transfected into COS-7 cells, and the cells were screened with 125I-

CC IL-8. The DNA sequence of isolated cDNA clone pRKS5B-IL8r1.1,

CC encoding human IL-8 receptor, is given in Q80520 and the predicted

CC amino acid sequence in R68811. The receptor is used to raise

CC antibodies that neutralize the activity of PF4AR, e.g. IL-8 receptor.

SQ Sequence 350 AA;

Query Match 9.1%; Score 325; DB 12; Length 350;

Best Local Similarity 31.3%; Pred. No. 4.21e-18;

Matches 47; Conservative 46; Mismatches 51; Indels 6; Gaps 6;

Db 43 iiayalvfllslgslmvlvlysvrsvtdvylnlaladllfaltlpiaaas-kvm 101

Qy 27 MWLSLTFLLGLPGNGLVWVAGL-KMORTVNTWFLHLTLADLLCCLSLAFSLAHIAIQ 85

Db 102 g-wifgtfclkvsvllkevnfygilllacisvdrylaivhatrtltqkth-lvkfvcqlg 159

Qy 86 GQMPYGRFLCKLIPSIIVLNMGFSVFLTAISLDRCLWFKP IWCQNHRNVGMCSIC-G 144

Db 160 c-wglamslpfflfrqayhpnnsqvcy 188

Qy 145 CIWVAFVLCIPVFVYREIFTTDDHNRGCGY 174

RESULT 12

ID R70123 standard; Protein; 1060 AA.

AC R70123;

DT 14-FEB-1996 (first entry)

DE IL8-R type 1-GBP 130 fusion protein.

KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;

KW red blood cell; cytokine receptor; glycophorin binding peptide 130;

KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.

OS Chimeric Homo sapiens.

OS Chimeric Plasmodium falciparum.

PN W09506737-A.

PD 09-MAR-1995.

PF 01-SEP-1994; G01900.

PR 03-SEP-1993; GB-018350.

PR 23-AUG-1994; GB-017021.

PA (PREN/) PRENDERGAST K F.

PI Prendergast KF;

DR WPI; 95-115452/15.

PT New hybrid peptide(s) for binding cytokine(s) - comprising a

PT malaria parasite peptide capable of binding a red blood cell and

PT a receptor peptide.

PS Example A; Page 79-80; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite

CC (Plasmodium falciparum) peptide (capable of binding to a red blood

CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples

CC of these hybrid peptides. R70123 is a fusion of interleukin 8 receptor

CC type 1 and glycophorin binding protein (GBP) 130. The use of cytokine

CC receptors not normally found on RBCs means that the cytokine can bind

CC harmlessly to the RBC without deleterious effect. The RBC protects the

CC hybrid peptides from excretion from the kidney, and due to steric

CC hindrance prevents the cytokines binding to a receptor in another cell.

CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides

CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),

CC PMSEA (pre major merozoite surface antigen) and the Duffy binding

CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides

CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on

CC the surface of RBCs. The hybrid peptides are thus used to lower

CC the levels of free cytokines in the circulation to reduce pathological

CC damage.

SQ Sequence 1060 AA;

Query Match 9.1%; Score 325; DB 14; Length 1060;

Best Local Similarity 31.3%; Pred. No. 4.21e-18;

Matches 47; Conservative 46; Mismatches 51; Indels 6; Gaps 6;

Db 43 iiayalvfllslgslmvlvlysvrsvtdvylnlaladllfaltlpiaaas-kvm 101

Qy 27 MWLSLTFLLGLPGNGLVWVAGL-KMORTVNTWFLHLTLADLLCCLSLAFSLAHIAIQ 85

Db 102 g-wifgtfclkvsvllkevnfygilllacisvdrylaivhatrtltqkth-lvkfvcqlg 159

Qy 86 GQMPYGRFLCKLIPSIIVLNMGFSVFLTAISLDRCLWFKP IWCQNHRNVGMCSIC-G 144

Db 160 c-wglamslpfflfrqayhpnnsqvcy 188

Qy 145 CIWVAFVLCIPVFVYREIFTTDDHNRGCGY 174

| SQ | Sequence | 428 AA; |
|----|----------|---------|
|----|----------|---------|

Qy 141 SICGCIWVAFVLCIPVFVYREI 163

Search completed: Wed May 1 15:29:13 1996
Job time : 58 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed May 1 15:31:03 1996; MasPar time 11.89 Seconds
Tabular output not generated.
Title: >US-08-462-355-2
Description: (1-482) from US08462355.pep
Perfect Score: 3591
Sequence: 1 MASFSAEIETNDLISQWNE.....TRSTHCPNNVISERNTTV 482
Scoring table: PAM 150
Gap 11
Searched: 43470 seqs, 15335248 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8
Statistics: Mean 50.162; Variance 95.878; scale 0.523
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result Query #
No. Score Match Length DB ID Description Pred. No.
1 601 16.7 352 1 C5AR CANFA CSA ANAPHYLATOXIN CHE 4.27e-95
2 580 16.2 350 1 C5AR HUMAN CSA ANAPHYLATOXIN CHE 1.03e-90
3 579 16.1 351 3 FML2 HUMAN FMLP-RELATED RECEPTOR 1.67e-90
4 555 15.5 347 1 C5AR MOUSE CSA ANAPHYLATOXIN CHE 1.63e-85
5 553 15.4 353 3 FML1 HUMAN FMLP-RELATED RECEPTOR 4.24e-85
6 536 14.9 364 3 FMLR MOUSE FMET-LEU-PHE RECEPTOR 1.41e-81
7 525 14.6 352 3 FMLR RABIT FMET-LEU-PHE RECEPTOR 2.64e-79
8 518 14.4 350 3 FMLR HUMAN FMET-LEU-PHE RECEPTOR 7.35e-78
9 391 10.9 359 1 AG2R WELGA TYPE-1 ANGIOTENSIN II 4.50e-52
10 369 10.3 362 1 AG2R XENLA TYPE-1-LIKE ANGIOTENS 1.05e-47
11 368 10.2 363 1 AG2S XENLA TYPE-1-LIKE ANGIOTENS 1.65e-47
12 357 9.9 359 1 AG2R HUMAN TYPE-1A ANGIOTENSIN I 2.44e-45
13 357 9.9 359 1 AG2R_PIG TYPE-1 ANGIOTENSIN II 2.44e-45

| | | | | | | | |
|----|-----|-----|-----|---|------------|-----------------------|----------|
| 14 | 356 | 9.9 | 359 | 1 | AG2R_BOVIN | TYPE-1 ANGIOTENSIN II | 3.84e-45 |
| 15 | 352 | 9.8 | 359 | 1 | AG2S_RAT | TYPE-1B ANGIOTENSIN I | 2.34e-44 |
| 16 | 350 | 9.7 | 359 | 1 | AG2R_RABIT | TYPE-1 ANGIOTENSIN II | 5.78e-44 |
| 17 | 346 | 9.6 | 359 | 1 | AG2S_MOUSE | TYPE-1B ANGIOTENSIN I | 3.51e-43 |
| 18 | 340 | 9.5 | 352 | 4 | LCR1_HUMAN | PROBABLE G PROTEIN-CO | 5.23e-42 |
| 19 | 338 | 9.4 | 359 | 1 | AG2R_MOUSE | TYPE-1A ANGIOTENSIN I | 1.28e-41 |
| 20 | 338 | 9.4 | 359 | 1 | AG2R_RAT | TYPE-1A ANGIOTENSIN I | 1.28e-41 |
| 21 | 335 | 9.3 | 355 | 4 | IL8B_HUMAN | HIGH AFFINITY INTERLE | 4.93e-41 |
| 22 | 332 | 9.2 | 353 | 4 | LCR1_BOVIN | PROBABLE G PROTEIN-CO | 1.89e-40 |
| 23 | 331 | 9.2 | 355 | 4 | IL8A_RABIT | HIGH AFFINITY INTERLE | 2.96e-40 |
| 24 | 325 | 9.1 | 350 | 4 | IL8A_HUMAN | HIGH AFFINITY INTERLE | 4.32e-39 |
| 25 | 315 | 8.8 | 418 | 7 | SSR3_HUMAN | SOMATOSTATIN RECEPTOR | 3.69e-37 |
| 26 | 314 | 8.7 | 380 | 1 | APJ_HUMAN | PROBABLE G PROTEIN-CO | 5.75e-37 |
| 27 | 312 | 8.7 | 428 | 7 | SSR3_RAT | SOMATOSTATIN RECEPTOR | 1.40e-36 |
| 28 | 311 | 8.7 | 428 | 7 | SSR3_MOUSE | SOMATOSTATIN RECEPTOR | 2.17e-36 |
| 29 | 308 | 8.6 | 363 | 7 | SSR5_RAT | SOMATOSTATIN RECEPTOR | 8.19e-36 |
| 30 | 308 | 8.6 | 400 | 5 | OPRM_HUMAN | MU-TYPE OPIOID RECEPT | 8.19e-36 |
| 31 | 306 | 8.5 | 398 | 5 | OPRM_RAT | MU-TYPE OPIOID RECEPT | 1.98e-35 |
| 32 | 295 | 8.2 | 358 | 4 | IL8B_RABIT | HIGH AFFINITY INTERLE | 2.50e-33 |
| 33 | 294 | 8.2 | 364 | 7 | SSR5_HUMAN | SOMATOSTATIN RECEPTOR | 3.87e-33 |
| 34 | 294 | 8.2 | 391 | 7 | SSR1_RAT | SOMATOSTATIN RECEPTOR | 3.87e-33 |
| 35 | 294 | 8.2 | 391 | 7 | SSR1_MOUSE | SOMATOSTATIN RECEPTOR | 3.87e-33 |
| 36 | 294 | 8.2 | 391 | 7 | SSR1_HUMAN | SOMATOSTATIN RECEPTOR | 3.87e-33 |
| 37 | 296 | 8.2 | 504 | 7 | TLR1_DROME | TACHYKININ-LIKE PEPTI | 1.61e-33 |
| 38 | 292 | 8.1 | 372 | 1 | BLR1_HUMAN | BURKITT'S LYMPHOMA RE | 9.29e-33 |
| 39 | 291 | 8.1 | 380 | 5 | OPRK_RAT | KAPPA-TYPE OPIOID REC | 1.44e-32 |
| 40 | 291 | 8.1 | 380 | 5 | OPRK_MOUSE | KAPPA-TYPE OPIOID REC | 1.44e-32 |
| 41 | 290 | 8.1 | 384 | 7 | SSR4_RAT | SOMATOSTATIN RECEPTOR | 2.23e-32 |
| 42 | 291 | 8.1 | 388 | 7 | SSR4_HUMAN | SOMATOSTATIN RECEPTOR | 1.44e-32 |
| 43 | 289 | 8.0 | 380 | 5 | OPRK_HUMAN | KAPPA-TYPE OPIOID REC | 3.45e-32 |
| 44 | 287 | 8.0 | 380 | 5 | OPRK_CAVPO | KAPPA-TYPE OPIOID REC | 8.25e-32 |
| 45 | 284 | 7.9 | 368 | 7 | SSR2_BOVIN | SOMATOSTATIN RECEPTOR | 3.05e-31 |

ALIGNMENTS

| | | | | |
|--------|---|-----------|------|---------------------------|
| RESULT | 1 | | | |
| ID | C5AR CANFA | STANDARD; | PRT; | 352 AA. |
| AC | P30992; | | | |
| DT | 01-JUL-1993 (REL. 26, CREATED) | | | |
| DT | 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) | | | |
| DT | 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE) | | | |
| DE | CSA ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (CSA-R). | | | |
| OS | CANIS FAMILIARIS (DOG). | | | |
| OC | EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; | | | |
| OC | EUTHERIA; CARNIVORA. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RM | 93111969 | | | |
| RA | PERRET J. J., RASPE E., VASSART G., PARMENTIER M.; | | | |
| RL | BIOCHEM. J. 288:911-917(1992). | | | |
| CC | -1- FUNCTION: RECEPTOR FOR THE CHEMOTACTIC AND INFLAMMATORY PEPTIDE | | | |
| CC | ANAPHYLATOXIN C5. THIS RECEPTOR STIMULATES CHEMOTAXIS, GRANULE | | | |
| CC | ENZYME RELEASE AND SUPEROXIDE ANION PRODUCTION. | | | |
| CC | -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. | | | |
| CC | -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. | | | |
| DR | EMBL; X65860; CFOMCSAM. | | | |
| DR | PIR; S27357; S27357. | | | |
| DR | GCROB; GCR 0558; -. | | | |
| DR | GCROB; GCR 0702; -. | | | |
| DR | PROSITE; P500237; G PROTEIN RECEPTOR. | | | |
| KW | G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; | | | |
| KW | CHEMOTAXIS. | | | |
| FT | DOMAIN 1 38 | | | EXTRACELLULAR (POTENTIAL) |

FT TRANSMEM 297 316 7 (POTENTIAL).
 FT DOMAIN 317 364 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 POTENTIAL.
 FT CARBOHYD 10 10 POTENTIAL.
 FT CARBOHYD 18 18 POTENTIAL.
 FT DISULFID 106 187 POTENTIAL.
 SQ SEQUENCE 364 AA; 40327 MW; 733437 CN;

Query Match 14.9%; Score 536; DB 3; Length 364;
 Best Local Similarity 43.4%; Pred. No. 1.41e-81;
 Matches 75; Conservative 54; Mismatches 38; Indels 6; Gaps 6;

Db 35 vfeylifavtvlqnglviwvqgmhktvtisylaladfcftstlpfysiam 93
 : : l : : : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Qy 24 ILSWVLSLTLFLGPGNGVLVWAGLKMQRVTWTFWHLTLADLLCCLSLAFSLAHL 82
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Db 94 vmqghwpfwmckfiyvtidlnlfgsvflialldrcicvhpwqnhrtvslakv 153
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Qy 83 ALQCCMPYGRFLCKLPSIIIVLMFGSVFLITAIISLDRCILWFKPIMQCNHRVGMACSI 142
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Db 154 iivpwicaflltlpvli-r-l-ttvmrqlg-pgktactfdfsp*tkdpvkr 202
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Qy 143 GCIIWVAFVLCIPVFVYREIFTDNHRCYKFGGLSSLDYDFYGDPLENR 195
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :

RESULT 7
 ID FMRL RABIT STANDARD; PRT; 352 AA.
 AC Q05394;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE FMET-LEU-PHE RECEPTOR (FMPL RECEPTOR) (N-FORMYL PEPTIDE RECEPTOR)
 DE (FPR).
 OS ERYCOTLAGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; LAGOMORPHA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=NEUTROPHILS;
 RM 93163563
 RA YE R.D., QUEHENBERGER O., THOMAS K.M., NAVARRO J., CAVANAGH S.L.,
 RA PROSSNITZ E.R., COCHRANE C.G.;
 RL J. IMMUNOL. 150:1383-1394(1993).
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
 CC FMPL TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- TISSUE SPECIFICITY: NEUTROPHILS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; M94549; OCPR.
 DR PIR; A46520; A46520.
 DR CCDB; CCR 0537; --.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW CHEMOTAXIS.
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 50 1 (POTENTIAL).
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 62 83 2 (POTENTIAL).
 FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 121 3 (POTENTIAL).
 FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 141 162 4 (POTENTIAL).
 FT DOMAIN 163 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 228 5 (POTENTIAL).
 FT DOMAIN 229 244 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 245 268 6 (POTENTIAL).
 FT DOMAIN 269 287 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 288 307 7 (POTENTIAL).
 FT DOMAIN 308 352 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 POTENTIAL.
 FT CARBOHYD 10 10 POTENTIAL.
 FT DISULFID 98 178 POTENTIAL.
 SQ SEQUENCE 352 AA; 38674 MW; 662482 CN;

Query Match 14.6%; Score 525; DB 3; Length 352;
 Best Local Similarity 47.3%; Pred. No. 2.64e-79;
 Matches 70; Conservative 44; Mismatches 31; Indels 3; Gaps 3;

Db 27 vfeylilvtfvlqnglviwvqgmhktvtisylaladfcftstlpfivtka 86
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Qy 24 ILSWVLSLTLFLGPGNGVLVWAGLKMQRVTWTFWHLTLADLLCCLSLAFSLAHL 83
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Db 87 lqghwpfwmckfiyvtidlnlfgsvflialldrcicvhpwqnhrtvslakvi 146
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Qy 84 LQCCMPYGRFLCKLPSIIIVLMFGSVFLITAIISLDRCILWFKPIMQCNHRVGMACSI 143
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Db 147 vgpwicallltlpvli-r-v-ttlehpr 171
 : : l : : l : : l : : : : l : : : : l : : : : l : : : : l : : : :
 Qy 144 GCIIWVAFVLCIPVFVYREIFTDNHNR 171

RESULT 8
 ID FMRL HUMAN STANDARD; PRT; 350 AA.
 AC P21462;
 DT 01-MAY-1991 (REL. 18, CREATED)
 DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE FMET-LEU-PHE RECEPTOR (FMPL RECEPTOR) (N-FORMYL PEPTIDE RECEPTOR)
 DE (FPR).
 GN FPRL.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 90267449
 RA BOULAY F., TARDIF M., BROUCHON L., VIGNAIS P.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 168:1103-1109(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RM 91105045
 RA BOULAY F., TARDIF M., BROUCHON L., VIGNAIS P.;
 RL BIOCHEMISTRY 29:11123-11133(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RM 91286286
 RA MURPHY P.M., MCDERMOTT D.;
 RL J. BIOL. CHEM. 266:12560-12567(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA PEREZ H.D.;
 RL SUBMITTED (MAR-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [5]
 RP SEQUENCE FROM N.A.
 RM 94040825

RESULT 10
 ID AG2R XENIA STANDARD; PRT; 362 AA.
 AC P32303;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE TYPE-1-LIKE ANGIOTENSIN II RECEPTOR 1 (AT1).
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 93343933
 RA JI H., SANDBERG K., ZHANG Y., CATT K.J.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 194:756-762 (1993).
 CC -/- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -/- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; L16463; XLANG2R.
 DR GCRDB; GCR 0693; -.
 DR PROSITE; P500237; G-PROTEIN RECEPTOR.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN;
 KW PALMITATE; PHOSPHORYLATION.
 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 53 1 (POTENTIAL).
 FT DOMAIN 54 65 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 66 88 2 (POTENTIAL).
 FT DOMAIN 89 103 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 104 125 3 (POTENTIAL).
 FT DOMAIN 126 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 144 163 4 (POTENTIAL).
 FT DOMAIN 164 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 215 5 (POTENTIAL).
 FT DOMAIN 216 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 295 7 (POTENTIAL).
 FT DOMAIN 296 362 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 3 3 POTENTIAL.
 FT CARBOHYD 18 18 POTENTIAL.
 FT CARBOHYD 177 177 POTENTIAL.
 FT DISULFID 102 181 BY SIMILARITY.
 FT LIPID 361 PALMITATE (POTENTIAL).
 SQ SEQUENCE 362 AA; 41039 MW; 735750 CN;

Query Match 10.3%; Score 369; DB 1; Length 362;
 Best Local Similarity 35.6%; Pred. No. 1.05e-47;
 Matches 52; Conservative 48; Mismatches 40; Indels 6; Gaps 6;
 Db 28 ifiaipilystifvqvgfmsvviyysymkm-ktvasiflmmlalsdl-cfvitiplw 85
 QY 23 VILSM-VILSTFLIGIPGNGVLWVA-G-LKQRTVNTWFLHLTLADLLC-CLSLAFS 78
 Db 86 aaytamhywpfnflekvaetaitlnlyttvfltlclsidrysaivhpmksriwtamv 145
 QY 79 LAHLALQOMPYGKFLCKLIPSIIVLNMFSGVFLTLTAISDLRCLVWFKPFWCONHRNVGM 138
 Db 146 arltcvqglwlvfaampsiirgdy 171
 QY 139 ACSICGCIWVAVVICIPVYREIF 164

RESULT 11
 ID AG2S XENIA STANDARD; PRT; 363 AA.
 AC P35373;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE TYPE-1-LIKE ANGIOTENSIN II RECEPTOR 2 (AT1).
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RM 93360920
 RA BERGSMAN D.J., ELLIS C., NUTHULAGANTI P.R., NAMBI P., SCAIFE K.,
 RA KOMAR C., AIYAR N.;
 RL MOL. PHARMACOL. 44:277-284 (1993).
 CC -/- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -/- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -/- TISSUE SPECIFICITY: HEART MEMBRANES, FOLLICULAR OOCYTES.
 CC -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U01155; XLI55.
 DR GCRDB; GCR 0763; -.
 DR PROSITE; P500237; G-PROTEIN RECEPTOR.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN;
 KW PALMITATE; PHOSPHORYLATION.
 FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 30 54 1 (POTENTIAL).
 FT DOMAIN 55 66 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 67 89 2 (POTENTIAL).
 FT DOMAIN 90 104 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 105 126 3 (POTENTIAL).
 FT DOMAIN 127 144 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 145 164 4 (POTENTIAL).
 FT DOMAIN 165 194 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 195 216 5 (POTENTIAL).
 FT DOMAIN 217 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 262 6 (POTENTIAL).
 FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 296 7 (POTENTIAL).
 FT DOMAIN 297 363 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT DISULFID 103 182 BY SIMILARITY.
 FT LIPID 346 346 PALMITATE (POTENTIAL).
 FT LIPID 362 362 PALMITATE (POTENTIAL).
 SQ SEQUENCE 363 AA; 41540 MW; 745704 CN;

Query Match 10.2%; Score 368; DB 1; Length 363;
 Best Local Similarity 34.4%; Pred. No. 1.65e-47;
 Matches 54; Conservative 51; Mismatches 44; Indels 8; Gaps 8;
 Db 29 ifitipilystifvqvgfmsvviyysymkm-ktmasvflmmlalsdl-cfvitiplw 86
 QY 23 VILSM-VILSTFLIGIPGNGVLWVA-G-LKQRTVNTWFLHLTLADLLC-CLSLAFS 78
 Db 87 aaytamhywpfnflekvaetaitlnlyttvfltlclsidrysaivhpmksriwtamv 146
 QY 79 LAHLALQOMPYGKFLCKLIPSIIVLNMFSGVFLTLTAISDLRCLVWFKPFWCONHRNVGM 138

Db 147 artlcvglwafllaelpsvlyqifipdntqva 183
 QY 139 ACSICGCIWVAVFLCIPVFVYREIFT-TD-NHRCG 173

RESULT 12
 ID AG2R HUMAN STANDARD; PRT; 359 AA.
 AC P30556;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE TYPE-1A ANGIOTENSIN II RECEPTOR (AT1A).
 GN AGTRI OR AT2RI.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 92337608
 RA MAUZY C.A., HWANG O., EGLOFF A.M., WU L.H., CHUNG F.-Z.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 186:277-284 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPHOCYTES;
 RM 92181475
 RA FURUTA H., GUO D.F., INAGAMI T.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 183:8-13 (1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RM 92231907
 RA BERGSMAN D.J., ELLIS C., KUMAR C., NUTHALAGANTI P., KERSTEN H.,
 RA ELSHOURBAGY N.A., GRIFFIN E., STADEL J.M., AIYAR N.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 183:989-995 (1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RM 92198490
 RA TAKAYANAGI R., OHNAKA K., SAKAI Y., NAKAO R., YANASE T., HAJI M.,
 RA INAGAMI T., FURUTA H., GOU D.F., NAKAMUTA M., NAWATA H.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 183:910-916 (1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RM 92375105
 RA CURNOW K.M., PASCOE L., WHITE P.C.;
 RL MOL. ENDOCRINOL. 6:1113-1118 (1992).
 CC -!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- TISSUE SPECIFICITY: LIVER, LUNG, ADRENAL, AND ADRENOCORTICAL
 CC ADENOMAS.
 CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; M91464; HSATIA.
 DR EMBL; Z11162; HSANTENIL.
 DR EMBL; M87290; HSANTIR.
 DR EMBL; M93394; HSANTIIR.
 DR PIR; A44014; A44014.
 DR PIR; JC1104; JC1104.
 DR GCRDB; GCR 0296; -.
 DR GCRDB; GCR 0384; -.
 DR GCRDB; GCR 0421; -.
 DR GCRDB; GCR 0447; -.

DR MIM; 106165; 11TH EDITION.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR.
 RW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN;
 KW PALMITATE; PHOSPHORYLATION.
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 52 1 (POTENTIAL).
 FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 65 87 2 (POTENTIAL).
 FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 143 162 4 (POTENTIAL).
 FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 193 214 5 (POTENTIAL).
 FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 262 6 (POTENTIAL).
 FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 296 7 (POTENTIAL).
 FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 POTENTIAL.
 FT CARBOHYD 176 176 POTENTIAL.
 FT CARBOHYD 188 188 POTENTIAL.
 FT DISULFID 101 180 BY SIMILARITY.
 FT LIPID 355 355 PALMITATE (POTENTIAL).
 SQ SEQUENCE 359 AA; 41061 MW; 712927 CN;

Query Match 9.9%; Score 357; DB 1; Length 359;
 Best Local Similarity 33.7%; Pred. No. 2.44e-45;
 Matches 56; Conservative 54; Mismatches 48; Indels 8; Gaps 8;

Db 27 ifvmtplysiifvvgifgnslvviyfyfymkltktvasvflnlaladl-cfllclplwa 85
 QY 24 ILSMV-IL-SLTFLGLPGNGLVWVAGIKMQ-RVTNTWFWLHFLTLADLCL-SLAFSL 79
 Db 86 vytameyrvpfnqylckiasaasfnlyasvfltlclslsldrylaivhpmksrlrrtmva 145
 QY 80 AHIALQCPMPYGRFLCKLIPSIIVLNFGSVLLTAISDRCLVWVFRPIWQCNHRNVGMA 139
 Db 146 kvctiilwllaglaaslpaiihrvnffientnitvcafhesqstl 191
 QY 140 CSICGCIWVAVFLCIPVFVYREIFTTDNHN-R-CGYKF-GLSSSL 182

RESULT 13
 ID AG2R PIG STANDARD; PRT; 359 AA.
 AC P30555;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE TYPE-1 ANGIOTENSIN II RECEPTOR (AT1).
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=AORTIC SMOOTH MUSCLE;
 RM 93259232
 RA ITAZAKI K., SHIGERI Y., FUJIMOTO M.;
 RL EUR. J. PHARMACOL. 245:147-156 (1993).
 CC -!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

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| CC | -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. |
| DR | EMBL; D11340; SSA2R. |
| DR | GRDB; GCR 0592; --. |
| DR | PROSITE; P500237; G PROTEIN RECEPTOR.. |
| DR | G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN; |
| KW | PALMITATE; PHOSPHORYLATION. |
| KW | |
| FT | DOMAIN 1 27 EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM 28 52 1 (POTENTIAL). |
| FT | DOMAIN 53 64 CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM 65 87 2 (POTENTIAL). |
| FT | DOMAIN 88 102 EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM 103 124 3 (POTENTIAL). |
| FT | DOMAIN 125 142 CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM 143 162 4 (POTENTIAL). |
| FT | DOMAIN 163 192 EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM 193 214 5 (POTENTIAL). |
| FT | DOMAIN 215 240 CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM 241 262 6 (POTENTIAL). |
| FT | DOMAIN 263 275 EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM 276 296 7 (POTENTIAL). |
| FT | DOMAIN 297 359 CYTOPLASMIC (POTENTIAL). |
| FT | CARBOHYD 4 4 POTENTIAL. |
| FT | CARBOHYD 176 176 POTENTIAL. |
| FT | CARBOHYD 188 188 POTENTIAL. |
| FT | DISULFID 101 180 BY SIMILARITY. |
| FT | LIPID 355 355 PALMITATE (POTENTIAL). |
| SQ | SEQUENCE 359 AA; 40906 MW; 730725 CN; |

[illegible]

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| RESULT | 14 |
| ID | AG2R BOVIN STANDARD; PRT; 359 AA. |
| AC | P25104; |
| DT | 01-MAY-1992 (REL. 22, CREATED) |
| DT | 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE) |
| DT | 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE) |
| DE | TYPE-I ANGIOTENSIN II RECEPTOR (AT1). |
| OS | BOS TAURUS (BOVINE). |
| OC | EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; |
| OC | EUTHERIA; ARTIODACTYLA. |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RM | 91251900 |
| RA | SASAKI K., YAMANO Y., BARDHAN S., IWAI N., MURRAY J.J., HASEGAWA M., |
| RL | MATSUDA Y., INAGAMI T.; |
| RA | NATURE 351:230-233(1991). |
| CC | -!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY |
| CC | ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL- |
| CC | CALCIUM SECOND MESSENGER SYSTEM. |

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|----|---|----------|---|
| CC | - | ! | TISSUE SPECIFICITY: ADRENAL MEDULLA, CORTEX, AND KIDNEY. |
| CC | - | ! | PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED. |
| CC | - | ! | SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. |
| CC | - | ! | SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. |
| DR | EMBL | X62294 | BTAA11TR. |
| DR | PIR | S15403 | S15403. |
| DR | GRDB | GCR 0372 | -. |
| DR | PROSITE | P500237 | G-PROTEIN_RECEPTOR. |
| KW | G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN; | | |
| KW | PALMITATE; PHOSPHORYLATION. | | |
| FT | DOMAIN | 1 | 27 |
| FT | TRANSMEM | 28 | 52 |
| FT | DOMAIN | 53 | 64 |
| FT | TRANSMEM | 65 | 87 |
| FT | DOMAIN | 88 | 102 |
| FT | TRANSMEM | 103 | 124 |
| FT | DOMAIN | 125 | 142 |
| FT | TRANSMEM | 143 | 162 |
| FT | DOMAIN | 163 | 192 |
| FT | TRANSMEM | 193 | 214 |
| FT | DOMAIN | 215 | 240 |
| FT | TRANSMEM | 241 | 262 |
| FT | DOMAIN | 263 | 275 |
| FT | TRANSMEM | 276 | 296 |
| FT | DOMAIN | 297 | 359 |
| FT | CARBOHYD | 4 | 4 |
| FT | CARBOHYD | 176 | 176 |
| FT | CARBOHYD | 188 | 188 |
| FT | DISULFID | 101 | 180 |
| FT | LIPID | 355 | 355 |
| SO | SEQUENCE | 359 AA; | 41088 MW; 724453 CN; |

| | | |
|---|--|---|
| | 9.9%; Score 356; DB 1; Length 359;
Best Local Similarity 33.7%
Matches 56; Conservative 54; Mismatches 48; Indels 8; Gaps 8; | |
| D | b | 27 ifimtiptlysiifwqifgnlvvviyfyfmklktvasfllnlaladl~cfltltpwa 85

 : : : :: :: : : : : : ::
Qy 24 ILSWV-IL-STFELGPGNGUWAGIKMQ-RTVNTWFHLTLADLCCCI-SIASFSL 79 |
| D | b | 86 vytameyrwpfgnyclkiassasfnlyasvflltciidrydylahvpkmksrlrtmlva 145

 :: : : : :: : : : : : : : : |
| Q | y | 80 AHUALAQOMPYGRFLCKLPISIVLINMGSEVLTAISDRCLWFKPIWCQNHRVMGA 139 |
| D | b | 146 kvteciiwltaglasptaihnrvffientnitvcayhesqmstl 191

 :: : : : : : : : : : : |
| O | v | 140 CSTICGCIGWAFAVLCTIPVEYREJFTTDNHN--R-CGYKF-GLISSSL 182 |

| RESULT | 15 | STANDARD; | PRT; | 359 AA. |
|--------|--|-----------|------|---------|
| ID | AC2S RAT | | | |
| AC | P29089; | | | |
| DT | 01-DEC-1992 (REL. 24, CREATED) | | | |
| DT | 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE) | | | |
| DT | 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE) | | | |
| DE | TYPE-1B ANGIOTENSIN II RECEPTOR (AT1B) (AT3). | | | |
| GN | AT1B. | | | |
| OS | RATTUS NORVEGICUS (RAT). | | | |
| OC | EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; | | | |
| OC | EUTHERIA; RODENTIA. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=SPRAGUE-DAWLEY; | | | |
| RM | 92183879 | | | |

Search completed: Wed May 1 15:31:40 1996
Job time : 37 secs.